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which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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/label= Prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                ALRLAGIGLOQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
                                                                                                                                                                                                                   181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
                                                                                                                                                                                                                                                                                                                SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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                                                                                                           1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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                                      Score 3135; DB 2;
Pred. No. 3.3e-190;
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/note= "N-myristoylation site"
                                                               0; Mismatches
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'label= Signal peptide
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                                      100.0%;
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Matches 598; Conservative
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ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO715; PRO1017; PRO1112; PRO509; PRO863; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation.
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                                                         RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE
                                                                      181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGFWVRE
                                                                                                                  241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL
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/note= "N-glycosylation site"
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/note= "signal sequence"
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/note= "leucine zipper"
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The present sequence represents a novel human polypeptide. The proceed fication describes novel polypeptides designated PRO21, PRO292, PRO327, PRO1215, PRO1414, PRO343, PRO345, PRO345, PRO1415, PRO1515, PRO1512, PRO1512, PRO1512, PRO5853 and PROS82. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in
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100.0%; Pred. No. 3.3e-190;
ive 0; Mismatches 0;
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/note="transmembrane domain"
519..525
/note="N-myristoylation site"
'note= "N-glycosylation site"
                       453. .457
/note= "N-glycosylation
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99WO-US028313.
99WO-US028409.
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/note= "N-
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Matches 598; Conservative
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Wood WI;
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  (GETH ) GENENTECH INC
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or liver tumor.
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                                      FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
                                                                                                                                                 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                    LITYRNI.SGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
                                                                                                                                       PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQV 540
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                                                                                                                                                                                    GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGFGLOSPLHAKPYI 598
                                                                            FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR
                                                                                                                                                                          GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
                                                                                                                                                                                                                                                                                                              Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
                                                                                                                                                                                                                                                                                              Human PRO protein, Seq ID No 104.
                                                                                                                                                                                                                                         AAU83643 standard; protein; 598
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2000WO-US020710.
2000US-0222425P.
2000US-0227133P.
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2000US-0220664P.
2000US-0220666P.
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2000WO-US034956.
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2001US-00854280.
2001WO-US017092.
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24-AUG-2000;
10-NOV-2000;
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20-DEC-2000;
20-DEC-2000;
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01-MAR-2001;
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22-AUG-2000;
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25-MAY-2001;
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in perioyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention
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                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
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Godowski PJ;
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   Goddard A, Goucher TF. Watanabe CK,
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                   Gerritsen ME, Goddard
Smith V, Stephan JF,
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Matches 598; Conservative
                          Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                     WPI; 2002-172001/22
                                                                                                                                                      N-PSDB; ABK33587
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New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
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 598
                541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLOSPLHAKPYI 598
GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLOSPLHAKPYI
                                                                                                                                                                                                                                             cytostatic; antiarteriosclerotic; antinflammatory; antidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer, atherosclerosis; inflammatory disease; diabetic complication; cardiac injury; organ failure.
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A, Godowski PJ, Grimaldi JC, Gurney AL,
Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                     Human; PRO; secreted protein; transmembrane protein; anti-HIV;
                                                                                                                                                                                                      Human secreted/transmembrane protein PR0357.
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                                                                                                       ABU55931 standard; protein; 598
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99WO-US012252
99WO-US021090
99WO-US028413
99WO-US028409
99WO-US028301
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28-JUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032678.
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2000WO-US004414.
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25-MAY-2001; 2001US-00866028
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1E, Goddard A,
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N-PSDB; ABX75493.
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15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
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16-DEC-1999,
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defined sequences of 957-3441 base pairs, given in the specification; or (c) at least 80% sequence identity to a full-length coding sequence of a DNA deposited under ATCC Accession No. 209526, 209508, 209508, 209530, 209532, 209532, 209531, 209529, 209577, 209570, 209508, 209531, 209521 or 209510, 209531, 209529, 209577, 209570, 209518, 209531, 209521 or 209619; (2) a vector comprising the nucleic acid; (3) a host cell comprising the vector which, when cultured under conditions suitable for expression of the PRO polypeptide, produces the PRO protein; (4) a chimeric molecule comprising PRO fused to a heterologous amino acid commerce, and (5) an anti-PRO antibody. The methods and compositions of the present invention are useful for the diagnosis and treatment of the present invention are useful for the diagnosis and treatment of disease, diabetic complications, cardiac injury and organ failure. The antibodies can also be used in the different screening, therapeutic and biological assays. The present sequence represents a PRO protein
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; Pred. No. 3.3e-190;
0; Mismatches 0;
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100.0%;
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Best Local Similarity 100.
Matches 598; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
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                                                                                                                                                                                                                                                                                                      useful for the manufacture of a medicament for diagnosing or treating
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                                                                                                                                                                                                                                                                                         twenty two nucleic acids encoding PRO
                                                                                                                                                                                                                    Goddard A,
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Pred. No. 3.3e-190;
; Mismatches 0;
                                                                                                                                                                                                                              Stephan JF,
                                                                                                                                                                                                                    Gerritsen ME,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                         28-AUG-2002; 2002US-00230163
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Best Local Similarity 100.
Matches 598; Conservative
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                                                                                                                                                                                           (GETH ) GENENTECH INC.
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                                                          US2003036635-A1.
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                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 250% or 1759 bp fully defined in the specification; or (b) any of 122 nucleotide sequences. The PRO POLYPEPTIGES or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte
                                                                                                                                                                                                                                                                                                                                                             598
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PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV
                                                                                                   LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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C, Gurney AL,
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cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumnours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDMA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility;
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Matches 598; Conservative
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use in
detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane polypeptides (e.g. PRO241, for use pharmaceuticals, diagnostics or bioreactors, particularly for deteror treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
birth defect, premature aging; diabetes; dog; cat; horse; acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit; industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-arteriosclerotic; antidabetic.
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PJ, Grimaldi JC, Gurney AL
Roy MA, Tumas D, Wood WI;
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970S-0069334P.
970S-0069425P.
970S-0069694P.
970S-0069694P.
970S-006966P.
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99WO-US012252.
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98US-0074092P.
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2000WO-US005841
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IE, Goddard
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                                                       Homo sapiens
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02-MAR-2000;
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Hillan KJ,
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22-JUN-1
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infertility, birth defects, premature aging, acquired immunodeficiency syndrome (ALDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
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Human secreted/transmembrane protein PRO357.
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ABUG4927
ABUG4927
ABUGAX
AC ABUG
AC AB
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Human, PRO; secreted protein, transmembrane protein; Cornella de Lange syndrome; gene therapy; immune disorder; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; cardiac injury; AIDS; cancer; diabetic complication.

Homo sapiens.

US2002173463-A1

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on DL, Ferrara N, Filvaroff E;
Godowski DJ, Grimaldi JC, Gurney
apier MA, Roy MA, Tumas D, Wood W
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ME, Goddard A, Godowski
Kljavin IJ, Napier MA,
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30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
28-UJL-2000; 2000WO-US022678.
28-FEB-2001; 2001WO-US035678.
                                      97US-0067411P
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                        2001US-00944944
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22-FEB-2000;
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Gerritsen
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chromosome New transmembrane polypeptides and polynucleotides useful for chromo identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers. N-PSDB; ABX96821.

Claim 12; Fig 26; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/transmembrane polypeptide (designated as PRO proteins). 15 PRO polypeptides and their encoding polynucleotides are disclosed. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the best cell under conditions for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture, an isolated polypeptide having at least 80% amino acid sequence identity to the PRO polypeptides, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence and an antibody which specifically binds to PRO. The PRO nucleotide sequences are useful as hybridisation probes, in chromosome and gene mapping, in generating sense and antisense RNA or DNA, in generating transgenic or knock-out animals which can be used in the development and screening of therapeutically useful reagents, and in gene therapy. The polypeptides may be used as molecular weight markers for protein electrophoreeis purposes. The PRO polypeptides and nucleic acids may also be used for chromosome identification, and tissue typing. US2002150976-A1.

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PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange syndrome. Other PRO proteins are variously implicated in immune disorders, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, cardiac injury, ALDS, cancer and diabetic complications. The present sequence represents
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New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
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Wood WI;
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Godowski PJ, Grimaldi JC, Gurn
apier MA, Roy MA, Tumas D, Woo
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Gerritsen ME, Goddard A, Godowski
Hillan KJ, Kljavin IJ, Napier MA,
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970S-0069334P
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Matches 598; Conservative
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N-PSDB; ABX78475.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HTV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
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A, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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100.0%; Pred. No. 3.3e-190;
ive 0; Mismatches 0;
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01-DEC-1999; 99WO-US028301.

16-DEC-1999; 99WO-US030095.

11-FEB-2000; 2000WO-US003565.

22-FEB-2000; 2000WO-US005411.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

28-JUL-2000; 2000WO-US020710.

28-FEB-2001; 2000WO-US032678.

28-FEB-2001; 2000WO-US02050.

25-MAY-2001; 2001WO-US0520.
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                    Kljavin IJ,
                                                                                                                                                                                                                                                 Botstein D,
E, Goddard
                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                      WPI; 2003-174140/17.
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                                                                                                                                                                                                                                                                                      Hillan KJ,
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61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPFNCVCPLSWFGPWVRE
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Matches 598; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 598 AA;
                                                                                                               Gerritsen ME,
                                                                                                                                 Hillan KJ,
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                                                                               PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQV 540
                                                                                                                                                      Human; PRO; antiinflammatory; antiarteriosclerotic; cardiant; gynecological; anti-HIV; cytostaric; antidiabetic; inflammatory disease; organ failure; arherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication.
                                                                                                                                                                                                            GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein, PRO357.
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97US-0069278P.
97US-0069334P.
97US-0069335P.
97US-0069425P.
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97US-0069702P.
97US-0069870P.
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99US-0146222P
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2000WO-US032678
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16-DEC-1997;
17-DEC-1997;
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18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
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22-DEC-1998;
02-JUN-1999;
28-JUL-1999;
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16-DEC-1997
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100.0%; Score 3135; DB 6; Length 598; 100.0%; Pred. No. 3.3e-190; Live 0; Mismatches 0; Indels 0

180 180 240 240 300

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The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to and scoring at least 80% positives when compared to any of 15 fully defined sequences of 235-954 amino acids, given in the specification. Also included are: (1) an isolated PRO compared to any of 15 fully defined mucleic acid sequence identity to a nucleotide sequence that encodes PRO or its extracellular domain, and comprising any of 15 fully defined nucleotide sequences of 957-3441 bp, given in the specification and deposited under ATCC accession number of your in the specification and deposited under ATCC accession number comprising the PRO nucleic acid; (3) a host cell comprising the vector; (4) producing PRO polypeptides, comprising the vector; (4) producing PRO polypeptides, comprising the PRO polypeptide and recovering the PRO polypeptide and comprising acid sequence; and (6) an anti-PRP antibody. The methods and compositions are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosoclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, diabetic complications and mutations in general. The present sequence is a a PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
                                                                                                                                                                                                                                    con DL, Ferrara N, Filvaroff E;
Godowski PJ, Grimaldi JC, Gurney AL
apier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                                                                                                                    Napier MA,
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28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
                                                                                                                                                                                                                                         Botstein D, Ea
ME, Goddard A,
                                                                                                                                                                                                                                                                                                                     Kljavin IJ,
                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-147446/14.
N-PSDB; ABX75940.
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The invention describes an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide (1) having at least 80 % cannot be a sign, 379, 984, 737, 433, 422, 300, 243, 455, 694, 440, 598, C26, 281, 431 or 235 amino acid sequence (31), given in the specification, S1 lacking its associated signal peptide or extracellular command of S1 withour without its associated signal peptide. (1) and the command of S1 without its associated signal peptide. (1) and the polymucleotide (II) encoding it are useful in tissue typing and gene thorwapy. (II) is also useful for generating transgenic animals or thorwapy and second animals for the development and screening of therapoutically cuseful reagents. PRO233 polypeptide is useful for treating inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, cuseful reagents. PRO233 polypeptide is useful for treating inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, control of processing processing and processing processing and processing proc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated PRO polypeptides e.g. PRO243, PRO399, PRO323, PRO327, PRO344, and polynucleotides useful in the treatment of human disorders related to immune system, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MCSRVPLLLPLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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                                                                                                                                                                                                                                                                           Saton DL, Ferrara N, Filvaroff E;
Godowski PJ, Grimaldi JC, Gurney AL
Napier MA, Roy MA, Tumas D, Wood WI;
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                                                                                                                                                                                                                                                                              Eaton DL,
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02-MAR-2000; 2000WO-US005841.
30-MAX-2000; 2000WO-US004939.
22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032679.
28-FEB-2001; 2000WO-US006520.
25-MAY-2001; 2001US-00866028.
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Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, N
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nes 598; Conservative
                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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                                                           Secreted and transmembrane polypeptide, PRO, tissue typing, gene therapy, transgenic; knockout animal; inflammatory disease, organ failure, atherosclerosis; cardiac injury; infertility; birth defect; premature aging; acquired immunodeficiency syndrome; AIDS; cancer; diabetic complication; immune system disorder; proteoglycan release; sports-related joint problem; human; articular cartilage defect; osteoarthritis; rheumatoid arthritis; vascular endothelial cell growth factor stimulated proliferation; endothelial cell growth; VEGF stimulated proliferation.
                                                                                                                                       PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
                                                                                                                                                                     PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAAILAAVGAAYCVRRGRAMAAAAQDKGQV 540
                                                                                                                                                                                                                                                                           GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPY1 598
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                            LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted and transmembrane protein PRO357.
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970S-0069334P.
970S-0069425P.
970S-0069694P.
970S-00696702P.
970S-0069870P.
970S-0069873P.
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970S-0069873P.
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98US-0075945P.
98WO-US019330.
98WO-US025108.
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98US-0112850P.
98US-00218517.
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99WO-US028409
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2000WO-US003565
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22-FEB-2000;
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09-FEB-1998;
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16-DEC-1997
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thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
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antiangiogenic; hypotensive; vulnenty; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertrension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
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                                                                              LIYRNISGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
                                                                                             481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . PJ;
Wood WI;
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                                                                                                                           PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV
                                                FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions,
                                                                                                                                                                                                                                                                                                                                                     secreted and transmembrane protein; PRO; cardiant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides
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a mammal.
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding useful in diagnosis and treatment of cardiovascular infarction), endothelial or angiogenic disorders in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen ME, Goddard Smith V, Stephan JF,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                          ABU82099 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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PRO323; PRO327; PRO333; PRO344; PRO347; PRO354; PRO355; PRO357; PRO715;
PRO353; PRO361; PRO365, gene therapy.
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useful for the affinity purification of PRO from recombinant cell culture or natural sources. The protein sequences and antibodies against them are useful for preparing a medicament treatment of a condition which is responsive to these. The present sequence represents a novel human protein sequence of the invention

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98WO-US025108.
98US-00216021.
98US-0112850P.
98US-00218517.
99US-00254311.
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2000WO-US020710.
2000WO-US032678.
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99WO-US028313.
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15-SEP-1999;
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Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI; Ferrara N, Eaton DL,

AL;

Filvaroff E;

Novel secreted and transmembrane polypeptides useful in tissue typing and preparing medicament for treating condition which is responsive to the

Claim 1; Fig 26; 172pp; English

This invention relates to the cDNA and protein sequences of a novel human secreted and transmembrane proceins such as RRO241, PRO343, PRO299, PRO313, PRO313, PRO314, PRO344, PRO344, PRO344, PRO355, PRO355, PRO353, PRO354, PRO354, PRO354, PRO355, PRO355, PRO357, PRO355, PRO353, PRO357, PRO354, PRO355, PRO355, PRO355, PRO357, PRO355, PRO3555, PRO3555, PRO3555, PRO3555, PRO3

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Matches 598; Conservative
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10000000000000000000000000000000000000	ULT 1 09-866-028-69 equence 69, Application U atent No. 6642360 ENERAL INFORMATION: APPLICANT: Bacter, Kevin APPLICANT: Betrara, Napol APPLICANT: Eaton, Dan APPLICANT: Eaton, Dan APPLICANT: Gerritsen, Mar APPLICANT: Gerritsen, Mar APPLICANT: Goddard, Audre APPLICANT: Goddard, Nath APPLICANT: Goddard, Nath APPLICANT: Goddard, Nath APPLICANT: Goddard, Nath APPLICANT: Majavin, Ivant APPLICANT: Kljavin, Ivant APPLICANT: Roy, Margaret APPLICANT: Roy, Margaret APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Roy, Margaret TITLE OF INVENTION: SECRE TITLE OF INVENTION: SECRE FILE REFERENCE: 25548P1CI CURRENT FILING DATE: 200	0. 69 PRT 1. 598 PRT 1. 598 1. 6089 1. 608
1488 1488 1490 1490 1490 1495 1498 1498 11998	RESULT 1 US-09-866-028-69 Sequence 69, Applicate Patent No. 6642360 GENERAL INFORMATION: APPLICANT: Baker, Kerara, APPLICANT: Baten, Da APPLICANT: Genteran, APPLICANT: Grimaldi APPLICANT: Grimaldi APPLICANT: Roy, Margham APPLICANT: Napier, MAPPLICANT: Napier, MAPPLICANT: Napier, MAPPLICANT: Napier, MAPPLICANT: Tumas, Da APPLICANT: Mood, Will TITLE OF INVENTION: TITLE OF INVENTION GA WILL TITLE OF INVENTION: TITL	NOTE
Sequence 6, Appli Sequence 7777, Ap Sequence 6, Appli Sequence 6, Appli Sequence 12902, A Sequence 21303, A Sequence 21303, A Sequence 21551, A Sequence 23551, A Sequence 2315, A Sequence 23, Appl Sequence 53, Appl Sequence 53, Appl Sequence 1663, A	Sequence 1855, Ap. Sequence 11, App. Sequence 87, Appl. Sequence 5, Appl. Sequence 10, Appl. Sequence 1009, Ap. Sequence 1009, Ap. Sequence 10, Appl. Sequence 5, Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 11, Appl. Sequence 1806, Appl. Sequence 11, Appl. Appl	Sequence 8, Appli Sequence 15, Appli Sequence 15, Appli Sequence 10, Appli Sequence 10, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 76, Appli Sequence 76, Appli Sequence 76, Appli Sequence 17, Appli Sequence 17, Appli Sequence 130, Appli Sequence 130, Appli Sequence 131, Appli Sequence 131, Appli Sequence 131, Appli Sequence 131, Appli Sequence 131, Appli Sequence 15, Appli Sequence 20280, A
US-09-566-047-6 US-09-966-047-6 US-08-9136-6 US-08-551-356-6 US-08-377-2858-40 US-09-377-2858-40 US-09-275-991A-27303 US-09-252-991A-27303 US-09-252-991A-27303 US-09-252-991A-28515 US-09-252-991A-28515 US-09-252-991A-28615 US-09-252-991A-28615 US-09-252-991A-28615 US-09-949-016-1351 Sequence US-09-949-016-1351	US-09-949-016-7855 US-09-809-016-7855 US-09-800-112 US-09-800-112 US-09-80-112 US-09-372-652-5 US-08-378-652-5 US-08-38-2 US-08-980-06-5 US-09-980-06-5 US-09-980-06-5 US-09-99-016-50909 US-09-949-016-11707 US-09-949-016-11709 US-09-949-016-77995 US-09-948-1113D-34 US-09-252-991A-20312 US-09-252-991A-20312 US-09-253-991A-20312 US-09-253-991A-18806 US-09-253-991A-18806 US-09-253-991A-18806 US-09-253-991A-18806 US-09-253-91A-18806 US-09-253-991A-18806 US-09-253-091A-18806 US-09-253-991A-18806 US-09-253-991A-18806 US-09-253-9	US-08-196-479B-8 Sequence US-08-196-479B-8 Sequence US-09-866-028-15 Sequence US-09-944-457-15 Sequence US-09-944-457-15 Sequence US-08-196-479B-10 Sequence US-08-18-191-10-10-45-3 Sequence US-08-440-816A-3 Sequence US-08-440-816A-3 Sequence US-09-22B-91A-28918 Sequence US-09-22B-986-76 Sequence US-09-22B-986-76 Sequence US-09-22B-986-76 Sequence US-09-318-092-874-8 Sequence US-09-949-016-7769 Sequence US-09-949-016-7769 Sequence US-09-945-041-130 Sequence US-09-35B-05B-131 Sequence US-09-35B-05B-131 Sequence US-09-35B-05B-131 Sequence US-09-32B-05B-131 Sequence US-09-32B-05B-13 Sequence US-09-32B-05B-15 Sequence US-09-93B-33B-15 Sequence US-09-93B-33B-15 Sequence US-09-32B-05B-15 Sequence
4 US-09-566-047-6 4 US-09-966-047-6 2 US-08-9116-777 2 US-08-551-356-6 5 PCT-US93-12687-6 5 PCT-US93-12687-6 6 US-09-377-2858-40 6 US-09-252-991A-27303 6 US-09-252-991A-27303 6 US-09-252-991A-28515 7 US-09-252-991A-28515 7 US-09-252-991A-2891 7 US-09-252-991A-2891 7 US-09-252-991A-2891 7 US-09-252-991A-2891 7 US-09-949-016-11663	Sednence se construction de la c	1 US-08-196-479B-8 Sequence 1 US-08-196-479B-8 Sequence 4 US-09-866-028-15 Sequence 4 US-09-966-028-15 Sequence 1 US-08-944-457-15 Sequence 1 US-08-944-457-15 Sequence 1 US-08-941-104A-3 Sequence 2 US-08-441-104A-3 Sequence 2 US-08-441-104A-3 Sequence 3 US-09-447-381A-3 Sequence 4 US-09-228-986-76 Sequence 4 US-09-228-986-76 Sequence 5 US-08-820-874-8 Sequence 6 US-08-323-474-8 Sequence 7 US-08-949-016-7769 Sequence 7 US-09-949-016-7769 Sequence 8 US-09-949-016-7769 Sequence 9 US-09-949-016-7769 Sequence 9 US-09-949-016-7769 Sequence 9 US-09-948-016-7769 Sequence 9 US-09-948-016-778-Sequence 9 US-09-958-0558-15 Sequence
2 1248 4 US-09-566-047-6 2 1254 4 US-09-566-047-6 2 1336 2 US-08-51-356-6 2 1336 2 US-08-551-356-6 2 1346 4 US-09-377-2858-40 2 1346 4 US-09-377-2858-40 2 1347 4 US-09-377-2858-40 2 234 4 US-09-252-991A-27303 2 234 4 US-09-252-991A-2851 2 233 4 US-09-252-991A-2851 2 339 4 US-09-252-991A-2821 2 339 4 US-09-252-991A-2827 2 334 4 US-09-252-991A-2827 2 344 4 US-09-249-016-11663 2 344 4 US-09-949-016-11663 2 Sequence 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	493 4 US-09-949-016-7855 Sequence 530 4 US-09-380-729-112 Sequence 619 2 US-08-80-729-112 Sequence 619 2 US-08-372-652-5 Sequence 619 2 US-08-372-652-5 Sequence 619 2 US-08-372-652-5 Sequence 619 2 US-08-980-060-5 Sequence 712 2 US-08-980-060-5 Sequence 712 2 US-08-980-060-5 Sequence 712 3 US-09-73-755-5 Sequence 713 3 US-09-73-755-5 Sequence 714 US-09-73-755-5 Sequence 715 4 US-09-73-755-5 Sequence 716 4 US-09-949-016-10832 Sequence 717 4 US-09-949-016-10832 Sequence 718 1 US-08-348-0068-5 Sequence 719 1 US-08-348-0068-5 Sequence 710 US-09-949-016-10832 Sequence 711 US-08-348-0068-5 Sequence 712 US-09-949-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-520-9999-016-7995 Sequence 718 US-09-252-991A-18806 Sequence 719 US-09-252-991A-18806 Sequence	2 708 1 US-08-196-479B-8 Sequence 2 708 1 US-08-818-823-8 Sequence 2 737 4 US-09-866-028-15 Sequence 2 737 4 US-09-866-028-15 Sequence 2 739 1 US-08-396-479B-10 Sequence 2 739 1 US-08-396-479B-10 Sequence 2 739 1 US-08-818-813-10 Sequence 2 814 2 US-08-841-104A-3 Sequence 2 814 2 US-08-441-104A-3 Sequence 2 18 4 2 US-09-417-381A-3 Sequence 2 18 5 US-09-228-986-76 Sequence 2 19 6 US-09-228-986-76 Sequence 2 1138 2 US-09-228-986-76 Sequence 2 1138 2 US-08-250-291A-588-76 Sequence 2 1138 2 US-08-250-291A-58 2 1138 2 US-08-250-291A-5 2 1138 2 US-08-250-291A-5 2 11429 3 US-09-949-016-7769 Sequence 2 1429 4 US-09-949-016-7769 Sequence 2 1429 4 US-09-945-016-7769 Sequence 2 1429 4 US-09-925-991A-50280 Sequence 2 7787 4 US-09-925-991A-50280 Sequence 2 7787 4 US-09-925-991A-50280 Sequence 2 7787 4 US-09-925-991A-50280 Sequence 3 178 4 US-09-252-991A-50280 Sequence
3.2 1248 4 US-09-566-047-6 3.2 1254 4 US-09-949-016-7777 Sequence 3.2 1336 2 US-08-551-356-6 3.2 1336 2 US-08-551-356-6 3.2 1336 5 PCT-US93-12687-6 3.2 1740 4 US-09-377-2858-40 3.2 1741 4 US-09-275-291A-27303 3.2 163 4 US-09-255-991A-27303 3.2 283 4 US-09-255-991A-28515 3.2 283 4 US-09-252-991A-28115 3.2 373 4 US-09-252-991A-28827 3.2 373 4 US-09-919-497-53 3.2 374 4 US-09-919-497-53 3.2 384 4 US-09-919-497-53 3.2 Sequence 3.2 373 4 US-09-919-497-53 3.2 Sequence 3.2 373 4 US-09-919-497-53 3.2 374 4 US-09-919-016-1351 3.2 Sequence 3.2 374 4 US-09-922-1002 3.2 Sequence	101 3.2 493 4 US-09-949-016-7855 Sequence 101 3.2 530 4 US-09-969-112 Sequence 101 3.2 540 4 US-09-862-8112 Sequence 101 3.2 519 4 US-09-538-092-817 Sequence 101 3.2 519 5 PCT-US95-15311-5 Sequence 101 3.2 712 1 US-08-980-060-5 Sequence 101 3.2 712 2 US-08-980-060-5 Sequence 101 3.2 712 2 US-09-99-919-185-5 Sequence 101 3.2 712 5 PCT-US96-09193-2 Sequence 101 3.2 712 5 PCT-US96-09193-2 Sequence 101 3.2 712 5 PCT-US96-09193-2 Sequence 101 3.2 725 4 US-09-949-016-6909 Sequence 101 3.2 725 4 US-09-949-016-6909 Sequence 101 3.2 1257 1 US-09-949-016-1707 Sequence 101 3.2 1257 1 US-09-949-016-8209 Sequence 101 3.2 1257 1 US-09-949-016-8209 Sequence 101 3.2 1911 2 US-09-949-016-8209 Sequence 101 3.2 1911 2 US-09-949-016-8209 Sequence 101 3.2 1911 5 PCT-US94-1016-5 Sequence 101 3.2 1911 5 PCT-US94-1016-5 Sequence 101 3.2 1911 5 PCT-US94-1016-5 Sequence 101 3.2 373 4 US-09-185-18-57-5 Sequence 101 3.2 373 4 US-09-185-18-67-5 Sequence 102 3.2 373 4 US-09-252-991A-1806 Sequence 103 3.2 373 4 US-09-252-991A-180	3.2 708 1 US-08-396-479B-8 Sequence 3.2 708 1 US-08-818-823-8 Sequence 3.2 737 4 US-09-866-028-15 Sequence 3.2 737 4 US-09-866-028-15 Sequence 3.2 737 4 US-09-944-457-15 Sequence 3.2 739 1 US-08-396-479B-10 Sequence 3.2 739 1 US-08-396-479B-10 Sequence 3.2 814 2 US-08-411-104A-3 Sequence 3.2 814 2 US-08-441-104A-3 Sequence 3.2 814 2 US-08-441-104A-3 Sequence 3.2 814 2 US-09-417-381A-3 Sequence 3.2 814 2 US-09-417-381A-3 Sequence 3.2 814 2 US-09-417-381A-3 Sequence 3.2 1138 1 US-09-52-991A-8918 Sequence 3.2 1138 2 US-09-22-91A-8918 Sequence 3.2 1138 2 US-09-240-464-6 Sequence 3.2 1138 2 US-09-549-016-7769 Sequence 3.2 1138 2 US-09-549-016-7769 Sequence 3.2 1138 2 US-09-549-016-7769 Sequence 3.2 11429 3 US-09-545-041-15 Sequence 3.2 787 4 US-09-925-991A-20280 Sequence 3.2 788 4 US-09-925-991A-20280 Sequence 3.2 788 4 US-09-925-991A-20280 Sequence 3.2 787 4 US-09-925-991A-20280 Sequence 3.2 787 4 US-09-925-991A-20280 Sequence 3.2 788 4 US-09-925-991A-20280 Sequence 3.2 362 905-9437-3 Se

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APPLICATION NUMBER: 60/070,440 FILING DATE: January 5, 1998 APPLICATION NUMBER: 60/074,086
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CURRENT PILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/66,028

PRIOR PLILNG DATE: 2001-05-25

PRIOR PLILNG DATE: December 11, 1997

PRIOR PLILNG DATE: December 12, 1997
                                                                                                   301 APIWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                                                             361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                                                                                                                 LIYRNISGPDKRLVILRLPASLAEYIVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
                                                                                                                                                                                                                                                                                             481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
                                                                                                                                                                                                                                                                                                                                                                                              481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
                                                                                                                                                                      FIGLYCESOMGOGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLORYLOGSSVOLRSLR 420
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APPLICATION NUMBER: 60/068,017
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PRIOR FILING DATE: December 16, 1997
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Patent No. 6734288
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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Napier, Mary
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100.0%; Pred. No. 1.8e-217;
cive 0; Mismatches 0;
PRIOR AFFLICATION NUMBER: 60/074,086
PRIOR PLING DATE: January 5, 1998
PRIOR PLING DATE: February 9, 1998
PRIOR PLING DATE: February 9, 1998
PRIOR PLING DATE: February 9, 1998
PRIOR PLING DATE: February 25, 1998
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PRIOR PLING DATE: December 16, 1998
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PRIOR PLING DATE: DECEMBER 16, 1998
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PRIOR PLING DATE: SEPTEMBER 197/US99/28113
PRIOR PLING DATE: DECEMBER 11, 1999
PRIOR PLING DATE: DECEMBER 19, 1099
PRIOR PLING DATE: DECEMBER 19, 1099
PRIOR PLING DATE: DECEMBER 16, 1999
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PRIOR PLING DATE: DECEMBER 16, 1999
PRIOR PLING DATE: PEDFUGATION NUMBER: PCT/US99/30095
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PRIOR PLING DATE: PEDFUGATION NUMBER: PCT/US90/064419
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PRIOR PLING DATE: PEDFUGATION NUMBER: PCT/US00/05411
PRIOR PLING DATE: PEDFUGATION NUMBER: PCT/US00/05419
PRIOR PLING DATE: PEDFUGATION NUMBER: PCT/US00/05419
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. 6734288ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. 6734288ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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   241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300
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Sequence 10, Application US/09520†81

Sequence 10, Application US/09520†81

FRICA TOPELL TANCRAMATION:

APPLICANT: Shimkers, Richard A.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY

FILE REPRENCE: 15966-540 No. 6689866el Polynucleotides

CURRENT PILING DATE: 2000-03-08.

PRIOR APPLICATION NUMBER: USSN 60/123,667

PRIOR APPLICATION NUMBER: USSN 60/123,667

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

TYPE: PRT

TYPE: PRT

ORGANISM: HOMO Sapiens
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17 ILLPFVXLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSN
                                                                                             TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC
                                                                                                                361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC
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                                                 7 LLLPLLLL------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD
                                  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT
                                                                                                                                                           HIGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL
                                                                                                                                                                                    421 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL
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Best Local Similarity
Matches 159; Conserv
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                                                                                                             SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
                                                                                                                              241 SHVTLASPEETRCHFPPRNAGRILLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09063950C
Patent No. 6225085
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1988-04-21
NUMBER OF SEQ ID NOS: 9
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                                                                      181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE
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ORGANISM: Homo sapiens
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US-09-063-950-2
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                                                                                                                                                    365 SEGRMAELKCRIPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTC 424
                                                                                                                                                                                                      -- LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP-- 383
                                                                                                                                                                                                                                             ----SFFTTGTGETTEISPEDTTRKY 473
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09063950C
Sequence 6.25085
GENERAL INFORMATION:
APPLICANT: HOALtzman.
APPLICANT: HOALtzman.
APPLICANT: HOALtzman.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
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                                                                              313 WWLRE-YIPINSTCCGRCHAPMHMRGRYLVEVDQASFOCSA-----PFIMDAPRDLNI
                                                                                                                        296 LSSSLAP-----TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC
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425 MGTNVAGNSNASAYLNGSTAELNTSNY----
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Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bostsein, David
APPLICANT: Bestsein, David
APPLICANT: Bestsein, David
APPLICANT: Bestoon, Dan L.
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; ORGANISM: Papio hamadryas
US-09-063-950-5
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    LIERNAFDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312
                                          PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
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Pred. No. 7e-16;
); Mismatches 187; Indels 126; Gaps
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS I
FILE REFERENCE: 15966-540 NO. 668986661 Polynucleotides
CURRENT APPLICATION NUMBER: US/09/520,781
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: USN 60/123,667
PRIOR FILING DATE: 1999-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 IGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAAR---
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Patent No. 6689866
GENERAL INFORMATION:
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25.8%;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.6
Best Local Similarity 25.8
Matches 130; Conservative
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TYPE: PRT
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258 YLQDN-QINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCDC 316
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                                                                                                                                                           139 HLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELRVDENRIAVISDM 198
                                                                                                                                                                                                                      128 GLQQLD---------EGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRL 169
                                                                                                                                                                                                                                                          170 RLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVC 229
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                                                  79 GFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQËNNIQTISRAALAQLLKLEEL 138
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                                                                                                           DLSQNQIASLRLP-----RLLLLDLSHNSLLALEPGI---LDTANVEALRLA---GL
ENGITMLDASSFAGLPGLQLL
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5. 6664376
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrara, Napoleone
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Ashkenazi, Avi
Botstein, David
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Gao, Wei-Qiang
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Eaton, Dan L.
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; Pred. No. 7e-15;
87; Mismatches 216; Indels 182;
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
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                                                                                   Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
                                                                                                                                                              Paul J.
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Best Local Similarity 22.4
Matches 140; Conservative
                                               Wei-Qiang
                                                                                                                                      Goddard, A.
                                                                                                                                                                                                                                                                                                                                    Pan, James
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290 VREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGT 349
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                                      ----APST---ASPTTOPPTLS-IPNP
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TITLE OF INVENTION: Acids Encoding the Same
                                                                                   350 RHHLACLCPEGFTGLYCESQMGQGTRPSPTP--
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                   507 LAAVLLAALAAVGAAYC---VRRGR 528
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-07-07
PAPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09902775A
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
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Ashkenazi, Avi
Botstein, David
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GENERAL INFORMATION:
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                                                                                                                              393 RSY----
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Acids Encoding the Same
                                                                      PRIOR FILLING DATE: 2001-07-12
PRIOR PELLING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR PELLING DATE: 1999-07-12
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
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PRIOR PELLING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR PLICATION NUMBER: PCT/US99/30911
PRIOR PLILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30919
                                                                                                                                                                                                                                                                                                                   OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR FILING DATE: 1999-09-15
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-10-05
OR APPLICATION NUMBER: PCT/US99/28214
OR FILING DATE: 1999-11-29
OR FILING DATE: 1999-11-29
OR FILING DATE: 1999-11-30
               FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
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PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
SEQ ID NO SEQ ID NOS: 423
LENGTH: 660
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Best Local Similarity 22.4%
Matches 140; Conservative
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; ORGANISM: Homo sapiens
US-09-905-125A-28
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
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FRIOR PILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-12-02
FRIOR FILING DATE: 1999-12-02
FRIOR FILING DATE: 1999-12-02
FRIOR PILING DATE: 1999-12-02
FRIOR PILING DATE: 1999-12-16
FRIOR PELLING DATE: 1999-12-16
FRIOR PELLING DATE: 1999-12-16
FRIOR PELLING DATE: 1999-12-03
FRIOR PILING DATE: 1999-12-03
FRIOR APPLICATION NUMBER: PCT/US99/30919
FRIOR PILING DATE: 1999-12-20
FRIOR FILING DATE: 1999-12-20
FRIOR FILING DATE: 1999-12-36
FRIOR FILING DATE: 1999-12-36
FRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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tewart, Timothy A.
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Hillan, Kenneth, J
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Mather, Jennie P.
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/3091
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 660
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Best Local Similarity 22.4<sup>§</sup>
Matches 140; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                            20 LIISLGLYSQVSKILACPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLYLHUNQINNA 78
                                                                                                                                                                      ----ENGITMLDASSFAGLPGLQLL 81
                                                                                                         13 LLLALGPGVQ-----GCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF----
                                                                              Gaps
                                                                         87; Mismatches 216; Indels 182;
                                              10.2%; Score 320; DB 4; Length 660; 22.4%; Pred. No. 7e-15;
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Patent No. 6767995
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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                                                           Best Local Similarity 22.4*
Matches 140; Conservative
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Ashkenazi, Avi
Botstein, David
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ORGANISM: Homo sapiens
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   ; ORGANISM: HON
US-09-906-700-28
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                                                                                                                                                                                                                          APPLICANT: Tunna, Dationa, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane I
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US (99/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PELLOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLOR DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
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PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PELLOR NUMBER: PCT/US99/28564
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PRIOR PELLOR NUMBER: PCT/US99/28564
PRIOR PELLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PELLOR NUMBER: PCT/US99/28564
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PELLOR NUMBER: PCT/US99/30099
PRIOR FILING DATE: 1999-12-02
PRIOR PELLOR NUMBER: PCT/US99/30099
PRIOR FILING DATE: 1999-12-02
                                                                                                                                                                          Timothy A.
                                                                                                     Paoni, Nicholas F.
Roy, Margaret Ann
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Tumas, Daniel
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128 GLQQLD--
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                                                  230 PLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPV 289
                                                                                                                 317 SIKWVTEWLKYIPSSL-NVRGFMCQGPEQVRGMAVRELNMNLLSCP--TTTPGLPLFTP- 372
                                                                                                                                                       290 VREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGT 349
                                                                                                                                                                                                                      -VTPRPPRSLTLGIEP 395
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                              170 RLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVC
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                                                                                                                                                                                                                      RHHLACLCPEGFTGLYCESQMGQGTRPSPTP----
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
Stewart, Timothy A
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                   393 RSY----
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170 RIAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVC 229
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22.4%; Pred. No. 7e-15;
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                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 2000-01-05
PRIOR SPELING DATE: 2000-01-05
NUMBER: PCT/US09/3099
                                                                                                              APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-00-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-29
FILING DATE: 1999-11-29
                      FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/20944
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Best Local Similarity 22.4*
Matches 140; Conservative
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CORGANISM: Homo sapiens
US-09-904-920A-28
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Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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Sao, Wei-Qiang
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Eaton, Dan L.
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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----VHSNHAPVTQAREGNLPLLIAPA 506
                                     488 TYRICLVPLDAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGL 546
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TYSVCVMPLGPGRVPEGEEA-CGEAHTPPA-
                                                                                                         : :: | :: | :: | 547 IGGAVIFVLVVLLSVFCWHMHKKGR 571
                                                                                                                                                                                                                            Sequence 6843, Application US/09949016 Patent No. 6812339
                                                                                 LAAVLLAALAAVGAAYC---VRRGR
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                               US-09-949-016-6843
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Best Local
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TYSVCVMPLGPGRVPEGEEA-CGEAHTPPA-----VHSNHAPVTQAREGNLPLLIAPA 506
432 VNDTSIQVSWLSLFTVMAYKLTWVKMGHSLVGG----IVQERIVSGEKQHLSLVNLEPRS 487
                                                                                                         TYRICLVPLDAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGL 546
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APPLICANT: Wood, William, I.
ATITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
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APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/23089
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PILING DATE: 1999-10-05
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                               507 LAAVLLAALAAVGAAYC---VRRGR 528
                                                                                                                                                                                                       547 IGGAVIFVLVVLLSVFCWHMHKKGR 571
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APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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PRIOR APPLICATION NUMBER: 05/0143,048
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
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PRIOR PILING DATE: 1999-12-07
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CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
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Grimaldi, Christopher
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                          Kenneth, J
                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni, Nicholas F
                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                              Gurney, Austin L.
Hillan, Kenneth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secreted TITLE OF INVENTION: Acids En
                                                                                                                                                                                                                                                                                                                                      Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                   Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                          Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                  Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 VREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 TYSVCVMPLGPGRVPEGEEA-CGEAHTPPA-----VHSNHAPVTQAREGNLPLLIAPA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 GFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAALAQLLKLEEL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 DLSQNQIASLRLP------RLLLLDLSHNSLLALEPGI---LDTANVEALRLA---GL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 GLQQLD---------EGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 RLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVC 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 RHHLACLCPEGFTGLYCESQMGQGTRPSPTP-------VTPRPPRSLTLGIEP 395
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999;
PRIOR APPLICATION NUMBER: PCT/US00/00219;
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 28
LENGTH: 660
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-909-064-28
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Best Local Similarity
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Search completed: May 12, 2005, 19:12:40 Job time : 69 secs

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Sequence 69, A. Sequence 69, A. Sequence 69, A. Sequence 69, A. Sequence 69, A. Sequence 69, A. Sequence 69, A. Sequence 104, Sequence 104, Sequence 104,
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US-09-944-914-69
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US-10-213-465-104
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-223-082-46 Sequence -142-889-350 Sequence -146-874-350 Sequence -147-497-350 Sequence -115-374-350 Sequence	52-375-350 52-377-350	52-388-350 52-391-350 52-399-350	56-848-350	57-794-350	57-796-350 50-500-350	21-046-350	23-214-350	25-805-350 24-821-350	52-385-350	52-396-350	53-552-350 Se	56-841-350	56-842-350 S	56-844-350 56-845-350	56-846-350	21-052-350	21-053-350 S	21-054-350	23-212-350 S	23-213-350 23-291-350	23-322-350	23-7/1-350 23-911-350	24-823-350	25-931-350 S	27-852A-350	127-900A-350 Sequence	31-820A-350	12-886-350 16-728-350 2	46-786-350	57-798-350	23-913-350 40-473-350	40-806-350 S	10-810-350 10-863-350	\$1-699-350 S	141-703-350 Sequenc 141-706-350 Sequenc	41-757-350 Se	41-762-350	42-429-350 Sequen	42-884-350 Se 43-027-350 Se	43-115-350 Sequen	44-958-350 Se	45-632-350 Sequen
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: BCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548PCI
CURRENT APPLICATION NUMBER: U$/09/24,449
CURRENT APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: December 3, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PULICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR PULING DATE: December 11, 1997
PRIOR PULING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/06935
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61 ENGITMLDASSFAGLPGLDLDLSQNQIASLRLPRLLLLDLSHNSLLALBPGILDTANVE 120
                                                                      ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
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Patent No. US20020102647A1
GENERAL INFORMATION:
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Botstein, David
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Napier, Mary
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REIOR FILING DATE: December 19, 1997
REIOR FILING DATE: December 19, 1998
REIOR PELICATION NUMBER: 60,014, 602
REIOR FILING DATE: Pebruary 9, 1998
REIOR PELICATION NUMBER: 60,113, 296
REIOR FILING DATE: December 16, 1998
REIOR PELICATION NUMBER: 60,113, 296
REIOR PELICATION NUMBER: 60,113, 296
REIOR REILCATION NUMBER: 60,113, 296
REIOR REILCATION NUMBER: 60,113, 296
REIOR REILCATION NUMBER: 60,128, 2018
REIOR APELICATION NUMBER: PCT/US99/28131
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CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-26
                                                                                           1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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                  598;
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100.0%; Scc. 100.0%; Pred. No. 1... 0; Mismatches
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PRIOR APPLICATION NUMBER: 09/866,028
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Patent No. US20020110859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
              Query Match
Best Local Similarity 100.
Matches 598; Conservative
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Hillan, Kenneth
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Tumas, Daniel
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APPLICATION NUMBER: PCT/US99/21090
PILING DAFE: September 15, 1999
PELING NUMBER: PCT/US99/28409
FILING DATE: No. US20020110859Alember 30, 1999
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FILING DATE: NO. US20020110859Alember 30, 1999
FILING DATE: DECEMBER: PCT/US99/28301
FILING DATE: DECEMBER!, 19999
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R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 60/113,296
R FILING DATE: December 22, 1998
R FILING DATE: December 22, 1998
R FILING DATE: July 28, 1999
R APPLICATION NUMBER: 60/146,222
R FILING DATE: July 28, 1999
R APPLICATION NUMBER: PCT/US98/19330
R APPLICATION NUMBER: PCT/US98/1930
R FILING DATE: December 1, 1998
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R APPLICATION NUMBER: PCT/US00/05841
R FILING DATE: March 2, 2000
R APPLICATION NUMBER: PCT/US00/08439
R FILING DATE: March 30, 2000
R APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
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FLIAND APPLI MATCH 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/US00/04414
FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069335
FILING DATE: December 11, 1997
                                                                              APPLICATION NUMBER: 60/069,278
FILING DATE: December 11, 1997
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APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
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APPLICATION NUMBER: 60/070,440
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APPLICATION WUMBER: 60/074,086
FILING DATE: FEBTUARY 9, 1998
APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/075,945
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FILING DATE: December 22, 1998
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FILING DATE: December 16, 1998
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APPLICATION NUMBER: 60/069,
FILING DATE: December 17, 1
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PRIOR APPLICATION NUMBER: PCT/USO1/06520 PRIOR FILING DATE: February 28, 2001 NUMBER OF SEQ ID NOS: 120 SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 69, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Best Local Similarity 100.0%;
Matches 598; Conservative (
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Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
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APPLICANT: Botstein, David
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                                                                                              TYPE: PRT
CRGANISM: Homo Sapien
US-09-944-457-69
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| THILE OF INVESTION IN ADDRESS AND TRANSMERGRAME POLYREPTIDES AND NUCLEIC TITLE OF INVESTION AND ADDRESS ENCODING THE SAME
| THILE OF INVESTION AND MURBER: 18/16/914/862
| CURRENT PAPILICATION WINDERS: 18/16/914/862
| PRIOR PALLICATION WINDERS: 18/16/91/862
8101
| PRIOR PALLICATION WINDERS: 18/16/91/862/8101
| PRIOR PALLICATION WINDERS: 18/16/91/862/8101
| PRIOR PALLICATION WINDERS: 18/16/91/862/8101
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FILING DATE: No. US20020127643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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                     Godowski, Paul
Grimaldi, Christopher
                                              Gurney, Austin
Hillan, Kenneth
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Tumas, Daniel
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PLING DATE: MAY 22, 2000
PRIOR FILING DATE: MJY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: DATY 20, 2000
PRIOR PILING DATE: PCT/US00/32678
PRIOR FILING DATE: PEDUARY 28, 2001
PRIOR FILING DATE: PEDUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
LENGTH: 598
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Patent No. US20020127643A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 598; Conservative
                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-69
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: 05/06/028
PRIOR PEDILICATION NUMBER: 05/06/028
PRIOR PEDILICATION NUMBER: 07/06/028
PRIOR PEDILICATION NUMBER: 07/06/03/134
PRIOR PELLING DATE: 2001-05-25
PRIOR PEDILICATION NUMBER: 60/06/13/19
PRIOR PELLING DATE: December 11, 1997
PRIOR PEDILICATION NUMBER: 60/06/27/19
PRIOR PELLING DATE: December 11, 1997
PRIOR PEDILICATION NUMBER: 60/06/27/19
PRIOR PELLING DATE: December 12, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/28
PRIOR PELLING DATE: December 12, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/28
PRIOR PELLING DATE: December 12, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/28
PRIOR PELLING DATE: December 16, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/29
PRIOR PELLING DATE: December 16, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/29
PRIOR PELLING DATE: December 16, 1997
PRIOR PEDILICATION NUMBER: 60/06/2/29
PRIOR PEDILICATION NUMBER: 60/06/2/29
PRIOR PEDILICATION NUMBER: 60/06/2/29
PRIOR PELLING DATE: December 16, 1997
PRIOR PEDILICATION NUMBER: 60/07/2/39
PRIOR PELLING DATE: December 16, 1997
PRIOR PEDILICATION NUMBER: 60/07/2/39
PRIOR PELLING DATE: PEDRUARY 5, 1998
PRIOR PELLING DATE: PEDRUARY 25, 1998
PRIOR PELLING DATE: PEDRUARY 25, 1998
PRIOR PELLING DATE: PEDRUARY 25, 1998
PRIOR PELLING DATE: PEDRUARY 26, 1999
PRIOR PELLING DATE: December 16, 1998
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PRIOR PELLING DATE: December 11, 1998
PRIOR PELLING DATE: DECEMBER: 09/254,311
PRIOR PELLING DATE: DECEMBER: 09/254,311
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Grimaldi, Christopher
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Filvaroff, Ellen
                                                        Baker, Kevin
Botstein, David
Eaton, Dan
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Goddard, Audrey
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Hillan, Kenneth
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Roy, Margaret
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Wood, William
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            PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: Pertuary 11, 2000
PRIOR FILING DATE: Pertuary 11, 2000
PRIOR APPLICATION NUMBER: PCT/USSO/0414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: Pebruary 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: JOUNDER: PCT/USSO/14042
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: Pebruary 26, 2001
PRIOR FILING DATE: Pebruary 26, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: PEBRUARY 28, 2001
PRIOR FILING DATE: PEBRUARY 28, 2001
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US-09-945-587-69
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Best Local Similarity
Matches 598; Conserv
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ò S C S-09-945-015-69 Sequence 69, Application US/09945015

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541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGFGLQSPLHAKPYI 598
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                                                            541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGFGCLQSPLHAKPYI
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CURRENT PELING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR PELING DATE: DECEMBER: 60/067,411
PRIOR PELING DATE: DECEMBER: 1,1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: DECEMBER: 11,1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR PILING DATE: DECEMBER: 11,1997
PRIOR PILING DATE: DECEMBER: 1,1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR PILING DATE: DECEMBER: 1,1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR PILING DATE: DECEMBER: 1,1997
PRIOR PILING DATE: DECEMBER: 1,1997
PRIOR PILING DATE: DECEMBER: 1,1997
PRIOR PILING DATE: DECEMBER: 1,1997
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PRIOR PILING DATE: DECEMBER: 1,1998
PRIOR PILING DATE: PEDTUARY 9, 1998
PRIOR PILING DATE: DECEMBER: 60/112, 296
PRIOR PELING DATE: DECEMBER: 60/112, 296
PRIOR PILING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
                                                                                                                                                                                                                                                   Sequence 69, Application US/09944396
Patent No. US20020132981A1
GENERAL INFORMATION:
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Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Roy, Margaret
Tumas, Daniel
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                                      IOR FILING DATE: September 15, 1999

IOR APPLICATION NUMBER: PCT/US99/28409

IOR FILING DATE: No. US20020132768alember 30, 1999

IOR APPLICATION NUMBER: PCT/US99/28313

IOR FILING DATE: No. US20020132768Alember 30, 1999

IOR APPLICATION NUMBER: PCT/US99/28301

IOR APPLICATION NUMBER: PCT/US99/30095

IOR APPLICATION NUMBER: PCT/US99/30095

IOR APPLICATION NUMBER: PCT/US99/30095

IOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. 10200201327684199
PRIOR FILING DATE: No. US2002013276841913
PRIOR FILING DATE: No. US2002013276841919
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PILING DATE: December 1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDCHARY 11, 2000
PRIOR FILING DATE: FEDLUARY 11, 2000
PRIOR FILING DATE: FEDLUARY 22, 2000
PRIOR FILING DATE: FEDLUARY 22, 2000
PRIOR FILING DATE: PEDCHARY 23, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/14042
PRIOR PLING DATE: DATE MARCH 30, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
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PRIOR FILING DATE: DECEMBER: PCT/US00/32678
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Best Local Similarity 100.
Matches 598; Conservative
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; ORGANISM: Homo Sapien
US-09-945-015-69
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CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PELING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069, 654

PRIOR PELING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069, 694

PRIOR PELING DATE: December 16, 1997

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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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APPLICANT: Botstein, David
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Napier, Mary
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Wood, William
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: December 12, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: SEPTEMBER: PCT/US99/22409
PRIOR FILING DATE: SEPTEMBER: PCT/US99/28409
PRIOR FILING DATE: SEPTEMBER: PCT/US99/28409
PRIOR FILING DATE: SEPTEMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR PILING DATE: No. US20020132981A1ember 30, 1999
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: PECT/US99/30095
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PRIOR PILING DATE: PECT/US00/0841
PRIOR PILING DATE: PEDTUATY 11, 2000
PRIOR PILING DATE: February 22, 2000
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PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR PILING DATE: MAY 28, 2000
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APPLICANT: ROY, MATGATECT
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
FRIOR FILING DATE: 2001-09-26
FRIOR APPLICATION NUMBER: 09/666,028
FRIOR FILING DATE: December 3, 1997
FRIOR APPLICATION NUMBER: 60/069,334
FRIOR FILING DATE: December 11, 1997
FRIOR PELING DATE: December 11, 1997
FRIOR FILING DATE: December 11, 1997
FRIOR PELING DATE: December 12, 1997
FRIOR PELING DATE: December 16, 1997
FRIOR PELING DATE: December 16, 1997
FRIOR APPLICATION NUMBER: 60/069,694
FRIOR PELING DATE: December 16, 1997
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FRIOR PELING D
                     301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
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Patent No. US20020142958A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Goddard, Audrey
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kijavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: JULY 28, 1999
PRIOR FILING DATE: JULY 28, 1999
PRIOR PLING DATE: September 16, 1998
PRIOR PLING DATE: September 16, 1998
PRIOR PLING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR PLING DATE: December 12, 1998
PRIOR PLING DATE: December 12, 1998
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PRIOR PLING DATE: December 15, 1999
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PRIOR PLING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US99/2801
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PLING DATE: December 16, 1999
PRIOR PLING DATE: December 16, 1999
PRIOR FILING DATE: PEDCUARTY 11, 2000
PRIOR PLING DATE: PEDCUARTY 22, 2000
PRIOR PLING DATE: MARCH 3, 2000
PRIOR PLING DATE: MARCH 3, 2000
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PRIOR PLING DATE: MARCH 3, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0520
PRIOR PLING DATE: MARCH 3, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0520
PRIOR PLING DATE: MARCH 3, 2000
PRIOR PLING DATE: MARCH 3, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0520
PRIOR PLING DATE: MARCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0520
PRIOR PRILING DATE: MARCH 30, 2000
PRIOR PRILING DATE: MARCH 30, 2000
PRIOR PRILING DATE: MARCH 2, 2000
PRIOR PRILING DATE: PEDCUARTY 28, 2001
PRIOR PRILING DATE: PEDCUARTY 28, 2001
PRIOR PRILING DATE: PEDCUARTY 28, 2001
PRIOR PRILING DATE: PEDCUARTY 28, 2001
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100.0%; Pred. No. 1.6
tive 0; Mismatches
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Matches 598; Conservative
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ORGANISM: Homo Sapien
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### APPLICATION NUMBER: 60/069,28

FILE REPREMENT SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREMENT: P248PICI
CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR PILING DATE: December 13, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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                                  181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
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Patent No. US20020142959A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christol
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Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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Tumas,Daniel
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                                     PRIOR FILING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 25, 1998
PRIOR PELING DATE: February 25, 1998
PRIOR PELING DATE: Pebruary 25, 1998
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PRIOR PELING DATE: DECEMBER: PCT/US99/1265
PRIOR PELING DATE: DECEMBER 10, 1999
PRIOR PELING DATE: New US20020142958Alember 30, 1999
PRIOR PELING DATE: PEPLUARY 22, 2000
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PRIOR PELING DATE: PEPLUARY 28, 2001
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PRIOR PELING DATE: PEPLUARY 28, 2001
PRIOR PEPLUARY 20, 2001
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100.0%; Pred. No. 1.6e-194;
tive 0; Mismatches 0;
      OR APPLICATION UNMBER: 60/074,096
OR APPLICATION NUMBER: 60/074,092
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: February 25, 1998
OR APPLICATION NUMBER: 60/112,850
OR FILING DATE: December:
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Best Local Similarity 100.
Matches 598; Conservative
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; ORGANISM: Homo Sapien
US-09-943-762-69
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APPLICANT: TUMAS, DATELL
APPLICANT: TUMAS, DATELL
APPLICANT: TUMAS, DATELL
APPLICANT: Wood, William
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/943,851A
CURRENT APPLICATION NUMBER: US/09/866,028
PRIOR PILING DATE: 2001-08-30
PRIOR PILING DATE: 2001-08-30
PRIOR FILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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                    61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Roy, Margaret
Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR FILING DATE: December 17, 1997

PRIOR FILING DATE: December 18, 1997

PRIOR FILING DATE: December 18, 1997

PRIOR FILING DATE: Pebruary 9, 1998

PRIOR FILING DATE: February 9, 1998

PRIOR FILING DATE: February 9, 1998

PRIOR FILING DATE: February 9, 1998

PRIOR PILING DATE: February 25, 1998

PRIOR PILING DATE: February 25, 1998

PRIOR PILING DATE: Pebruary 26, 1998

PRIOR PILING DATE: Pebruary 26, 1998

PRIOR PILING DATE: Pebruary 26, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PILING DATE: December 17, 1998

PRIOR PILING DATE: December 17, 1999

PRIOR APPLICATION NUMBER: PCT/US99/2819

PRIOR PILING DATE: December 15, 1999

PRIOR PILING DATE: MARCH: 3, 1999

PRIOR PILING DATE: SEPCEMBER: PCT/US99/2819

PRIOR PILING DATE: PEBRUARY 11, 2000

PRIOR PILING DATE: PEBRUARY 22, 2000

PRIOR PILING DATE: PEBRUARY 22, 2000

PRIOR PILING DATE: PEBRUARY 22, 2000

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR APPLICATION NUMBER: PCT/US99/279

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR APPLICATION NUMBER: PCT/US99/279

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR APPLICATION NUMBER: PCT/US90/0919

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR APPLICATION NUMBER: PCT/US90/0919

PRIOR PELING DATE: PEBRUARY 22, 2000

PRIOR PELING DA
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Pred. No. 1.6e-194;
; Mismatches 0;
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; ORGANISM: Homo Sapien
US-09-944-654-69
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Best Local Similarity
Matches 598; Conserv
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CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-26
                                                                                                            1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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Query Match 100.0%; Score 3135; DB 9; Best Local Similarity 100.0%; Pred. No. 1.6e-194; Matches 598; Conservative 0; Mismatches 0;
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Patent No. US20020156004A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Kljavin, Ivar
Napier, Mary
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Patent No. US20020165143A1
GENERAL INFORMATION:
  ; PRIOR FILING DATE: February 28, 20; NUBER OF SEQ ID NOS: 120; SEQ ID NO 69; LENGTH: 598; TYPE: PRT ORGANISM: HOMO Sapien US-09-944-413-69
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
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APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christol
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Best Local Similarity 100.
Matches 598; Conservative
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Hillan, Kenneth
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Napier, Mary
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Tumas,Daniel
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COR APPLICATION NUMBER: 09/218,517

COR FILING DATE: December 22, 1998

COR FILING DATE: March 3, 1999

COR FILING DATE: March 3, 1999

COR FILING DATE: March 3, 1999

COR FILING DATE: June 22, 1999

COR FILING DATE: SEPTEMBER: PCT/US99/21090

COR FILING DATE: SEPTEMBER: PCT/US99/28409

COR APPLICATION NUMBER: PCT/US99/28409

COR APPLICATION NUMBER: PCT/US99/28409

COR APPLICATION NUMBER: PCT/US99/28409

COR APPLICATION NUMBER: PCT/US99/28313

COR FILING DATE: No. US20020156004Alember 30, 1999

COR FILING DATE: NO. US20020156004Alember 30, 1999

COR APPLICATION NUMBER: PCT/US99/28301
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RAPLICATION NUMBER: 60/112,850

RFILING DATE: December 16, 1998

RFILING DATE: December 22, 1998

RFILING DATE: December 22, 1998

RAPLICATION NUMBER: 60/146,222

RAPLICATION NUMBER: PCT/US98/19330

RAPLICATION NUMBER: PCT/US98/19330

RAPLICATION NUMBER: PCT/US98/25108

RAPLICATION NUMBER: PCT/US98/25108

RAPLICATION NUMBER: PCT/US98/25108

RAPLICATION NUMBER: PCT/US98/25108

RAPLICATION NUMBER: 90/216,021
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/USO0/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USO0/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/USO0/14042
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US01/06520
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FILING DATE: December 16, 1997
Application.
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APPLICATION NUMBER: 60/070,440
ELING DATE: January 5, 1986
APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
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FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,278
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APPLICATION NUMBER: 60/069,425
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/075,945
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61 ENGITMIDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLLDLSHNSLLALEPGILDTANVE 120
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100.0%; Pred. No. 1.6e-194;
ive 0; Mismatches 0;
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PECT/US01/06520
PRIOR PELING DATE: FEDURATY 28, 2001
PRIOR FILING DATE: FEDURATY 28, 2001
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Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Best Local Similarity 100.
Matches 598; Conservative
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LENGTH: 598
TYPE: PRT
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                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,403

CURRENT APPLICATION NUMBER: US/09/944,403

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 16, 1997

PRIOR PLING DATE: December 16, 1997

PRIOR FILING DATE: December 17, 1997

PRIOR FILING DATE: December 17, 1997

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OR APPLICATION NUMBER: 09/254,311

OR FILING DATE: March 3, 1999

OR APPLICATION NUMBER: PCT/US99/12252

OR FILING DATE: June 22, 1999

OR PELING DATE: June 22, 1999

OR FILING DATE: September 15, 1999

OR FILING DATE: PCT/US99/28409

OR FILING DATE: PCT/US99/28409

OR FILING DATE: PCT/US99/28419

OR FILING DATE: PCT/US99/28419

OR FILING DATE: PCT/US99/28313

OR FILING DATE: PCT/US99/28313

OR FILING DATE: PCT/US99/28313

OR PILING DATE: PCT/US99/28313
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PRIOR PELING DATE: December 60/074,086
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 25, 1998
PRIOR PELING DATE: February 25, 1998
PRIOR PELING DATE: PECEMBER 60/11, 296
PRIOR PELING DATE: PECEMBER 16, 1998
PRIOR PELING DATE: PECEMBER 16, 1998
PRIOR PELING DATE: December 17, 1998
PRIOR PELING DATE: December 17, 1998
PRIOR PELING DATE: December 17, 1999
PRIOR PELING DATE: December 17, 1999
PRIOR PELING DATE: September 19, 1999
PRIOR PELING DATE: NOW UNBER: PCT/US99/28301
PRIOR PELING DATE: NOW US20020165143A.ember
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PRIOR PELING DATE: PEDRUARY 11, 2000
PRIOR PELING DATE: PEDRUARY 11, 2000
PRIOR PELING DATE: PEDRUARY 22, 2000
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FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/USOO/05841
FILING DATE: MARCH 2, 2000
APPLICATION NUMBER: PCT/USOO/08439
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61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRPRLILLDLDLSHNSLLALEPGILDTANVE 120
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Pred. No. 1.6e-194;
                                                                                                                                                                                                                                                                                100.0%; Scc...
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0; Mismatches
                 PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: PECT/US00/32678
PRIOR PILING DATE: PECT/US01/06520
PRIOR PILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
LENGTH: 598
APPLICATION NUMBER: PCT/USO0/04414
FILLING DATE: February 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 598; Conservative
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapien
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Gurney, Austin
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Roy, Margaret
Tumas, Daniel
Wood, William
                                                            Kljavin, Ivar
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                                     APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020173463Alember 30,
APPLICATION NUMBER: PCT/US99/28301
              US20020173463Alember 30,
PRIOR FILING DATE: No. US20020173463Alember 3
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020174463Alember 3
PRIOR FILING DATE: No. US20020174463Alember 1
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDTUATY 11, 2000
PRIOR PILING DATE: FEDTUATY 22, 2000
PRIOR PILING DATE: FEDTUATY 22, 2000
PRIOR FILING DATE: PEDTUATY 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: PEDTUATY 28, 2001
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; ORGANISM: Homo Sapien
US-09-944-944-69
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FILE REPERENCE: P2548P1C1.
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT RILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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PRIOR PRILING DATE: December 11, 1997
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FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
APPLICATION NUMBER: PCT/US99/28409
APPLICATION NUMBER: PCT/US99/28409
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR PILING DATE: MARCH 29,1311
PRIOR FILING DATE: MARCH 3, 1999
PRIOR FILING DATE: MARCH 3, 1999
PRIOR FILING DATE: JUME 22, 1999
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PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: Pebruary 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/112,296
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PRIOR PRILING DATE: JOHNBER: 60/070,440
PRILOR PLILING DATE: JANUARY 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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FILING DATE: December 17, 1997
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APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: 60/069,69
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APPLICATION NUMBER: 60/069,
FILING DATE: December 17, 1
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Grimaldi,Christopher
                                                                    Perrara, Napoleone
                                                                                              Filvaroff, Ellen
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Hillan, Kenneth
                                                                                                                           Gerritsen, Mary
                                                                                                                                                     Goddard, Audrey
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Roy, Margaret
Tumas, Daniel
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A;Molecule type: mRNA; protein A;Residues: 1-605 <leo> A;Cross-references: UNIPROT:P35</leo>	A, Mc	high-methionine d- leucine-rich repea mucin like protein	T02262 T07079 PC2022	000	209 221 235	0.00 0.00	6 6 6 6 6 6	1487 1488 1489
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tle: Structure and function	A,Ti	hypothetical prote	T33247		2109	90.	 	9 00 0
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ternate names: Acid-Lab:	N,A	protein F12M16.30	A96574		854	9.0	. m	-
115 Jing Jike arowth factore	A41915	subtilisin-like pr hymothetical prote	T05840		718	0.6	m m	7 4
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		hypothetical prote	T18116		577	w	m' m	72
244 LOKLYLDRNLIAAVAPG	qu	serine/threonine p	T42100		556	9.0		17
215 LRLLAAARNPFNCVCPL	ò	probable serine/th	T36501 a53437		522	w w	٠. س د	69
2	3	internalin G [impo	AG1107		490	0.0	 n	68
		hypothetical prote	B87335		458	0.0	m r	99
156 VP-PVIRGLRGLTRLRL	ò	transcription fact	150702		391	9.0	. m	65
127 LHLBRNQLRSLAVGTF	QQ .	probable cell wall	T06482		352	9.0	س د	163
99 LDLSHNSLLALEPGILD	λσ —	probable mmpS3 pro hvpothetical prote	G70784 T46721		299 305	o o	ო ო	161
0	3	bypothetical prote	T27610		278	. o	. n	160
	7 1	hypothetical prote	T30074		2153	0.0	۰,	158
46 VPRDVPPDTVGI,YVFRN	è	glutamate synthase hvnothetical profe	T11974 T00080		1560	o 0.	y 9 4 4	157
8 LALALLLSWYALGPRS	qa	gene expanded prot	T13720		1429	90.	46	122
	è	mannan endo-1,4-be racGAP protein - в	A48954 T18289		1335	9 0. 9 0.	y 9 4 4	4 5
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cession: JC5239	A, Ac	fasciclin II precu	A40114		898	9.0	40	144
nterence number: 003239; ontents: liver	A; S	interleukin-3 rece	A40091		878	0. m	9	143
tle: The cloning and expres	A,T	major nitrogen reg	S51493		862	9.0	46 0	141
them. Biophys. Res. Commun	Biod	probable transmemb	T36581		811	3.0	94	140
scession: JC5239	C; Ac	serine/threonine-s	A41090 S67265		793		9 9 4 4	9 6
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llin-like growth factor aci	insi P. C	neu differentiatio	161719 S50856		639 648	0 0	96 94 44	32
JC5239		hypothetical prote	B36789		590	3.0	94	134
. H.	1588	nucleoporin p62 -	S41819 C75286		522	0 O	y 0	333
		merozoite surface	B44997		476	3.0	94	131
		early growth respo	A40492 A36389		4 4 6 6	0 0 n m	y 9 4 4	30
		robable cel	T38309		421	9.0	94	128
93 3.0		nypornerical proce T8K14.10 [imported	A96826		356	9.0	94	127
93 3.0		probable cell surf	S28004 S76923		338 346	9 6	2, Q	25.5
93 3.0		cytokinin-induced	T10064		329	0.0	400	124
95 93 3.0		hypothetical prote hypothetical prote	E/2564 T22919	N (1	293) O	y 0	123
94 93 3.0		interleukin 15 rec	S57346	~ ~	7 0	ю. 0.0	46	121
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	C;Species: C;Date: 17 C;Accessic	-Apr-1 n: JC5	вр. (ра 997 #яед 239	neuce	rev	ision 09-	. (babbon) #sequence_revision 09-May-1997 #text_change 09-May-1997
	R, Delhanty Biochem. E A, Title: 1	, P.; Hophys he clo	Baxter, . Res. C ning and	R.C. Ommun. expre	22 1881	7, 897-90 on of the	R.Delhanty, P.; Baxter, R.C. Biochem. Biophys. Res. Commun. 227, 897-902, 1996 A.Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
e ABC trans ukin-3 rece	A; Referenc A; Contents	e numb	er: JC52 r	39, MU	ID:	97040714;	
	A; Molecule	n: JC5 : type:	239 mRNA 5 / DEL				
	C; Comment:	This	factori	s stru	ctn	rally rel	structurally related to proinsulin and have insuline-like metał
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iption fact	λ̈́σ	156 VP	- PVIRGLR	GLTRLR	I.AG	NTRIAQLRP	VP-PVIRGLRGLRELRELAGNTRIAQLRPEDLAGLDVSNLSLQALPGDLSGLFPR 214
ecrosis fac	qq	185 LP	DAAFRGLG	GLRELV	TAG-	N-RLAYLQP	LPDAAFRGLGGLRELVLAGN-RLAYLQPALFSGLAELRELDLSRNALRAIKANVFAQLPR 243
e serine/th	ò	215 LR	LILAAARNP 	FNCVCP	LSW	LRILAAARNPENCVCPLSWFGPWVRESHVTLA	RESHVTLA 246
threonine p	q _Q	244 LQ	KĽYLDŘŇL	IAAVAP	GAF	LOKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVA	DLSHNRVA 279
r-like prot i	RESULT 2						
	A41915 insulin-li	ke gro	wth fact	or-bin	din	g complex	acid-labile chain precursor - human
F12M16.30	N, Alternat C, Species:	e name Homo	s: Acid-	Labile (man)	Su	bunit (AL	3)
prote bindi	C;Date: 31	-Dec-1	993 #seq 915	nence	rev	ision 31-l	Dec-1993 #text_change 09-Jul-2004
	R; Leong, S	.R., B	axter, R	C., C	аше	rato, T.;	T.; Dai, J.; Wood, W.I.
	A,Title: SA,Reference	tructu e numb	re and f er: A419	unctio	nal ID:	expressic 92357025;	on of the acid-labile subunit of the insulin-lipMID:1379671
52 [im prote	A; Accessic A; Status:	n: A41 prelim	915 inary	•			
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A; Residues: 412-427 <RES>
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A; Cross-references: UNIPROT: P07359; GB: J02940; NID: g183499; PIDN: AAA52595.1; PID: g306793
A; Cross-references: UNIPROT: P07359; GB: J02940; NID: g183499; PIDN: AAA52595.1; PID: g306793
R; Wicki, A.N.; Walz, A; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J
Thromb. Haemost. 61, 448-453, 1899
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A:Reference number: A60435, MUID:90020160; PMID:2799758
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<LRR7>
<LRR7>
<LRR8>
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                                                                                           F;12-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;121-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;195-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;294-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;315-318/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;315-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;413-488/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;483-488/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;483-488/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;893-50/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;893-50/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;893-50/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;807-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRI F;807-
                                                                      F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology
A;Note: sequence extracted from NCBI backbone (NCBIP:1101/1)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 302; DB 2; Length 605;
; Pred. No. 3.7e-10;
40; Mismatches 98; Indels
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A;Residuee: 207-467 <WIC>
R;Titani, K:, Takio, K:; Handa, M:; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
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Best Local Similarity 35.5
Matches 98; Conservative
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C; Genetics:
A;Genetics:
A;Genetics:
C; Genetics:
C; Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)
C; Complex: heterodimer with platelet glycoprotein; platelet membrane; tandem repet C; C; Complex: heterodimer with platelet glycoprotein; glycoprotein; platelet membrane; tandem repet C; Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repet C; Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repet F;17-626/Product: platelet glycoprotein in papat chain #status predicted <MPT>
F;17-626/Product: platelet glycoprotein repeat homology <LRR1>
F;24-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;19-430/Region: proline/threonine-rich 9-residue repeat homology <LRR7>
F;379-430/Region: proline/threonine-rich 9-residue repeat F;510-430/Region: proline/threonine-rich 9-residue repeats
F;522-540/Domain: intracellular #status predicted <IRN>
F;541-626/Domain: intracellular #status predicted <IRNP
F;541-626/Domain: intracellular #status predicted <IRNP
F;541-626/Domain: intracellular #status predicted <IRNP
F;541-626/Domain: intracellular #status predicted <IRNP
A, Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet memt A, Reference number: A94173; MUD:87289654; PMID:3497398
A, Recession: A94173; MUD:87289654; PMID:3497398
A, Rocession: A94173; MUD:87289654; PMID:3497398
A, Molecule type: protein
A, Rolecule type: protein
A, Residues: 17-315 < TIT>
R, Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
A, Fits and Biochem: 199, 389-393, 1991
A, Title: Identification of the disulphide bonds in human platelet glycocalicin.
A, Reference number: S16945; MUID:91301149; PMID:2070794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates C;Comment: Platelet activation apparently involves disruption of the macromolecular compl C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with unl C;Comment: Glycocalicin, which is approximately coextensive with the extracellular part c
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J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number
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24.0%; Pred. No. 5.4e-09;
iive 72; Mismatches 244; Indels 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: I55355; MUID:92250564; PMID:1577776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Residues: 224-227;262-270;277-282
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Local Similarity 24.0%
hes 160; Conservative
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acid la

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111-1 protein homolog - rat

N.Alternate names: MEGF4 protein

N.Alternate names: MEGF4 protein

C.Species: Rattus norregicus (Norway rat)

C.Species: Rattus norregicus (Norway rat)

C.Accession: T42218

R.Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs I A;Reference number: Z14126; MUID:9836089; PMID:9693030

A;Accession: T42218

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1531 cMRA

A;Residues: 1-1531 cMRA

A;Residues: 1-1531 cMRA

A;Cross-references: UNIPROT:088279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g34

A;Experimental source: strain Sprague-Dawley; brain

C;Genetics:

A;Gene: MEGF4

C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re
                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g162161 C; Comment: This protein is a serum protein and it is of the ternary complex in the physic
                                                                                                                                                                                                                      mouse
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                                                                                                                              C;Accession: JCG128
R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Tille: Organization and chromosomal localization of the gene encoding the A;Reference number: JCG128; MUID:96413591; PMID:8816745
A;Accession: JCG128
                                                                      insulin-like growth factor binding complex acid labile chain - mouse C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 -PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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32.8%; Pred. No. 8.3e-09;
ive 48; Mismatches 101;
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25.8%; Pred. No. 2.5e-08;
ative 56; Mismatches 207;
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Matches 90; Conserv
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A; Residues: 1-603 <BOI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fact
A;Reference number: JC1282, MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-603 -CDAI>
A;Residues: 1-603 -CDAI>
A;Residues: 1-603 -CDAI>
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205 F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
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                                               273 YKYPGKGCPTLGDEGDTDLYDYYPEEDTEGDKVRATRTVVKFPTKAHTTPWGLFYSWSTA 332
                                                                                               ----APSPPSTAPPTVGPV---PQ 330
                                                                                                                           333 SLDSQMPSSLHPTQESTKEQTTFPPRWTPNFTLHMESITFSKTPKSTTEPTPSFTTSEPV 392
                                                                                                                                                                                        PQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLT 390
                                                                                                                                                                                                                                        393 PEPAPNMITLEPIP-----SPTIPE------PISEPAPSPITPET 431
                                                                                                                                                                                                                                                                                        LGIEP---VSPTSLRVGLQRYLQGSS--VQLRSLRLTYRNLSGPDKRLVTLR--LPASLA 443
                                                                                                                                                                                                                                                                                                                                   IATSPIILVSATSLITPKSTFLTTKPVSLLESTKKTIPELDQPPKLRGVLQGHLESSRN 491
                                                                                                                                                                                                                                                                                                                                                                                        ---PGRV-PEGEEACGEAHT 480
                                                                                                                                                                                                                                                                                                                                                                                                                      : | | : : : | | D---PFLHPD----FCCLLPLGFYVLGLFWLLFASVVLILLLSWVGHVKPQALDSGQGAAL 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAVHSNHAPVTQAREGNLP---LLI----APALAAVLLAALAAVGAAYCVRRGRAMAAA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 TTATQTTHLELQRGRQVTVPRAMLLFIRGSLPTFRSSLFLWVRPNGRVGPLVAGRRPSAL 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| |:| | |:| | :: | :: : :::| | | |:| | :: | | | |:| EDDIPUSTRALWILDGINILSSIPSAAPQNILSSIDFLNI,QGSWIRSIBPQALIGIQNILYYL 127
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-HFPPKNAGRLLLE--LDYADFGCPATTTTATVPTTRPVVREP
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32.4%; Pred. No. 5.6e-09;
tive 49; Mismatches 106;
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                                                                                          296 LSSSLAPTWLSPTAPATE---
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Db 176 VELILN-HIVPPEDERQNRSFEGWYVAALLAGRALQGLRRLELASN-HFLYLPRDVLAQL 233 Qy 189 AALQELDVSNLSLQALP	RESULT 8 T13953 MEGFS protein - rat N.Alternate names: slit protein homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T13953 R;Nakayama, M:; Nakajima, D:; Nagase, T:; Nomura, N:; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998 A;Ritle: Identification of high-molecular-weight proteins with multiple EGF-like motifs PA;Reference number: Z14126; MUID:98360089; PMID:9693030 A;Reference number: Z14126; MUID:98360089; PMID:9693030 A;Recession: T13953 A;Rodecular-weight proteins with multiple EGF-like motifs PA;Residues: 1-1253 < NAKA A;Residues: 1-1253 < NAKA A;Coss-references: UNIPROT:088280; EMBL:AB011531; NID:g3449291; PIDN:BAA32461.1; PID:g34 C;Genetics: A;Genetics: A	Ouery Match Best Local Similarity 26.3%; Score 261; DB 2; Length 1523; Best Local Similarity 26.3%; Pred. No. 2.4e-07; Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14; Qy 24 CPSGCQCSQPQTVPCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDL 83	Oy 263 LLLELDYADFGCPATTTATVPTRRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAP 322
Db 16 PELWILLWAAAWRLGATACPALCTCT-GTTVDCHGTGLQAIPKNIPRNTERLELNGNNIT 74 66 MLDASSFAGLPGLQLLDLSONOIASLRLPRLLLLDLSHNSLLALEPGIL-DTANVEALRL 124 1	OY 244 TLASPEETRCHPPRANAGRILIELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPT 303	ASS51 Oncofetal trophoblast glycoprotein 5T4 precursor - human NyAlternate names: oncofetal antigen 5T4 C; Species: Homo sapiens (man) N; Alternate names: oncofetal antigen 5T4 C; Species: Homo sapiens (man) C; Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 C; Accession: AS351; s40087 C; Merers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L. J; Biol. Chem. 269, 9319-9324, 1994 A; Fitle: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen A; Reference number: A53531; MUID: 94179356; PMID: 8132670 A; Accession: A53531 A; Assidues: 1-420 cMEY A; Molecule type: mRNA A; Residues: 1-420 cMEY A; Coss-references: UNIRROT: 013641; EMBL: Z29083; NID: 9435654; PIDN: CAA82324.1; PID: 94356 A; Cross-references: UNIRROT: 013641; EMBL: Z29083; NID: 945564; PIDN: CAA82324.1; PID: 94356 F; 1-31/Domain: signal sequence #status predicted cSIG> F; 32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted cMAT>	Query Match 8.4%; Score 264.5; DB 2; Length 420; Best Local Similarity 28.1%; Pred. No. 3.5e-08; Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15; Qy 2 CSRVPLLLPLLLLALG

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C,Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; $13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Derg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
A;Title: alit: an extracellular protein necessary for development of midline glia and com A;Reference number: A36665; MUID:91099665; PMID:2176636
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A; Introns: 1351/3

C; Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein regeat alternative splicing; growth factor.

E; & Wowdreis alternative splicing; growth factor.

F; & Wowdreis alternative splicing; growth factor.

F; & Wowdreis alternative splicing; growth factor.

F; & Womain: proteoglycan amino-terminal homology cLRR1>
F; 101-124 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR2>
F; 149-172 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 173-196 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR4>
F; 173-196 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
F; 173-196 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
F; 133-46 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 131-346 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR9>
F; 131-346 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR9>
F; 131-346 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR9>
F; 131-346 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR9>
F; 131-346 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
F; 135-317 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
F; 135-318 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
F; 137-35 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
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F; 137-35 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
F; 138-60-64 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
F; 138-60-64 (Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR19>
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R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of A;Reference number: A31640; MUID:89077533; PMID:314436
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A;Molccule type: DNA
A;Residues: 881-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RO2>
A;Residues: B81-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RO2>
A;Cross-references: GB:M23543; NID:g340939; PID:g514357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 255.5; DB 2;
21.4%; Pred. No. 4.8e-07;
tive 52; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 CPSGCQCSQPQTVFCTARQGTTVPRDVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: FlyBase:sli
;Cross-references: FlyBase:FBgn0003425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:1028-1061/Domain: EGF homology <EGF>F:1068-1099/Domain: EGF homology <EGFZ>F:1115-1148/Domain: EGF homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                         :|| ||::
977 YTGARCETNI 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1480 <ROT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A36665
                                                                                                                                                                                                                                                                                                                                                                  slit protein 1
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Best Local S
Matches 105
                                               361
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                                                                                                                                                                                                                                                                                                                                                                                                       protein; EGF homology; leucine-rich alpha-2-glycoprotein
                                                                                                                                                                                                                                                                                      A; Genee: FlyBase:sli
A; Gross-references: FlyBase:FBgn0003425
C; Superfamily: Fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycopy
F; 66-91/Domain: proteoglycan amino-terminal homology cpAH1>
F; 101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR1>
F; 102-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR2>
F; 149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F; 197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
F; 288-313/Domain: proteoglycan amino-terminal homology cPCS1>
F; 288-313/Domain: proteoglycan amino-terminal homology cPCS1>
F; 288-313/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR5>
F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR8>
F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR8>
F; 371-394/Domain: proteoglycan carboxyl-terminal homology cPCS2>
F; 371-394/Domain: proteoglycan carboxyl-terminal homology cLR19>
F; 596-643/Domain: proteoglycan carboxyl-terminal homology cPCS3>
F; 596-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR15>
F; 596-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR15>
F; 596-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR15>
F; 596-643/Domain: proteoglycan carboxyl-terminal homology cPCS3>
F; 700-790/Domain: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 LKRNQLTGIEPNAFEGASHIQELQLGENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VEALRLAGIGLOQLDEGLFSRLRNLHDLDV--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 638 SFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 ----- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                698 EFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAETSELYLESNEIEQI 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 HYERIRHLRSLTRLDLS-NNQITILSNYTFANLTKLSTLIISYNKLQCLQRHALSGLNNL 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          874 RCAEPEOMKDKLILSTPSSSFVCRGRVRNDILAKCNACFEOPCONQAQCV----ALPQ 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 TEAPSPPSTAPPTVGPVPQP------QDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              928 REYQC------LCQPGYHGKHCEFMIDACYGNPCRNNATCTVLEEGRFSCQCAPG 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLOALPGDLSGLFPR-----LRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEET 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PDTVGLY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Mismatches 168; Indels 165; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IRGLRGLTRIRLAGNTRIAQLRPEDLAGLAALQELDVS-
Reference number: A36665; MUID:91099665; PMID:2176636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 255.5; DB 2;
Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 CPSGCQCSQPQTVFCTARQGTTVPRDVP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1028-1061/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1115-1148/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 105; Conservative
                                                                                                                                                                     Residues: 1-1469 <ROT>
Cross-references: GB:X53959
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ILDTAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                    preliminary
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QY 162 GLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGD	RESULT 12 NBHUA2 leucine-rich alpha-2-glycoprotein - human C;5pscies: Homo sapiens (man) C;5pscies: Homo sapiens (man) C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Dec-1998 C;Accession: A0321 R;Takahashi, N.; Takahashi, Y.; Putnam, F.W. Proc. Natl. Acad. Sci. U.S.A. 82, 1906-1910, 1985 A;Title: Periodicity of leucine and tandem repetition of a 24-amino acid segment in the A;Reference number: A03211; MUID:85166241; PMID:3856868 A;Molecule type: protein A;Molecule type: protein A;Residues: 1-312 < TAKA>	C. Superfamily: leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein repeat homology cLRR1>	DD 5 PKDCQVFRSDHGSSISCQPPAEIPGYLPADIVHLAUFFNLTHLPANLLG 54 QY 74 GLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEA 121 DD 55 GASKLQELHLSSNGLESLSPEFLRPVPQLRVLDLTRNALTGLPPGLPQASATLDTLVLKE 114 QY 122
Oy 59 VFENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPG 112	S	RESULT 11 JC7973 synleurin - human C;Species: Homo sapiens (man) C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003 C;Accession: JC7973 B;Wang, W.; Yang, Y.; Li, L.; Shi, Y. Biochem. Biophys. Res. Commun. 305, 981-988, 2003 A;Title: Synleurin, a novel leucine-rich repeat protein that increases the intensity of A;Reference number: JC7973; PMID:12767927 A;Accession: JC7973 A;Residues: 1-622 «WAN> A;Residues: 1-622 «WAN> A;Coss-references: GB:AY280614 C;Comment: This protein that is a single span transmembrane leucine-rich repeat protein e intensity of pleiotropic cytokine responses as an adhesion protein or a receptor. A;Gene: slrn A;Map position: Sq12.1 C;Keywords: cytokine; leucine-rich repeat; synleurin; transmembrane protein	Query Match 8 .0%; Score 251; DB 2; Length 622; Best Local Similarity 23.1%; Pred. No. 3.3e-07; Matches 107; Conservative 52; Mismatches 142; Indels 162; Gaps 13; Cy 2 CSRVDLLLPLLLLALGEGVQCCSGCQCSQPTVFCTARQGTTVPRDVPDTVGLYVE 61 Db 10 CLRLFLVVTCYLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPETVFLYTG 69 Cy 62 NGITMLDASSFAGLPCLLDLSQNQIASIRLPRLLLLDSHNSLLALEPG 112 Db 70 NNISYINESELTGLHSLVALYLDNSNILYVVPRAFVQLRHLYFLFLNNFIRLDPGIFK 129 Cy 113

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	Db 127 LFLDHNALRGIDQNMFQKLV	LFLDHNALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLP 186
DD 283 KUKMFSQNDTKCAGPEAVKGQTLL 306	Ov 111 PGILDT-ANVEALRLAGLGLOOLDEGI	OOLDEGLFSRLRNIHD 145
RESULT 13	187	2 S. ING. PAGA ENGLANDING SALES ING. PAGA ENGLANDED SALES ING. PAGA EN
A60164		
piateiei membrane giycoprocein v precursor - numan C;Species: Homo sapiens (man)	Oy 146 LDVS	
C;Date: 12-Jan-1993 #sequence_revision_24-Feb-1994 #text_change_09-Jul-2004 C:Accession: A48030: A60164: A35483: R35483: C35483: A60439: A4507: S34229	Db 247 LTLSRNHLAFLPSALFLHSH	247 ÍTLSRNHLAFIPSALFIHSHNITLITLFENÞLAELÞGVIFGEMGGLQELMINRTQLRTLP 306
RiLanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T	Qy 163LRGLTRLRGNTR	LRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDV
9. BIOL: CHEW. 200, 20001-2000/, 1993 A; Title: Cloning and characterization of the gene encoding the human platelet glycoprote	Db 307 AAAFRNLSRLRYLGVTLSPR	307 AAAFRNLSRLKYLGVTLSPRLSALPQGAFQGLGELQVLALHSNGLTALPDGLLRGLGKLR 366
A;Reference number: A48030; MUID:94012616; PMID:8407908 A:Accession: A48030	.WS 791	SNISI-OAL-PGDI-SGI-PPRI-RII-AAARNPFNCV 228
A; Molecule type: DNA		
A; Kesidues: 1-560 <la2> A; Cross-references: UNIPROT: P40197; EMBL: Z23091; NID: 9312501; PIDN: CAA80637.1; PID: 93129</la2>	Db 367 QVSLRRNRLRALPRALFRNL	QVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCD 426
R;Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama,	Oy 229 CPLSWFGPWVRESHVTLASP	CPLSWFGPWVRESHVTLASPEB-TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTR 287
BIOGN 75, 2343-2356, 1990 A; Title: Rapid purification and characterization of human platelet glycoprotein V: the a	Db 427 CGLGPFLGWLRQ-HLGLVGG	
A;Reference number: A60164; MUID:90275263; PMID:2350580 A:Accession: A60164	ds.TWTGA.TSS.TATGHGARAYAY	700 GOVERNMENT OF THE PROPERTY
A; Molecule type: protein	0 0	
Ajkesidues: 365-384, X., 386-390, X.,392-395, X.,39/j188-208, T.,210/27-50, X.,52-55,174- ,'XX',108, T.;61-72, TK',75-77; V',56-57; G',479-487, X',489-498, X',500, X',502-503, X'	DD 4/9 FPRPANDSSS	EAFVHFALAFNSSEF 503
R;Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A. Biochem. Biophys. Res. Commun. 170, 153-161, 1990	RESULT 14	
A. Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a	JC7763	4000
A.P.C.E.G.C.C. Mander: A33403, NULL.3021120, FRID:23/2204 A;ACCESSION: A3483	neuronai reucine-iron repeat proce C;Species: Rattus norvegicus (Norw	in's - iac ay rat)
A; Molecule type: protein A: Pesidhes: 145-166 'T' 168-169 'X' 171-172 /POT>	C;Date: 01-Feb-2002 #sequence_revi	sion 01-Feb-2002 #text_change 09-Jul-2004
A; Note: this proteolytic fragment was designated peptide M392	R;Fukamachi, K.; Matsuoka, Y.; Kit	anaka, C.; Kuchino, Y.; Tsuda, H.
A;Accession: B35483 A:Molecule type: nortein .	Biochem. Biophys. Res. Commun. 287 A.Title: Rat neuronal leucine-rich	, 257-263, 2001 repeat protein-3: Cloning and regulation of the gene 6
A; Residues: 121-129, W', 131-135, 466-468, 'X', 470 <ro2></ro2>	A; Reference number: JC7763; PMID:1)
A;Note: unis material was designated peptide M393 but may contain two peptides A;Accession: C35483	A;contents: Fibrosarcoma cells A;Accession: JC7763	
A:Molecule type: protein A:Besidnes: 252-266 'H' 268-272 'X' 274-279 'T' 281-284 'T' 286 <803>	A.Molecule type: mRNA A.Residues: 1-707 <fuk></fuk>	A;Molecule type: mRNA A:Residues: 1-707 <ftk></ftk>
A, Note: this proteolytic fragment was designated peptide M401	A; Cross-references: UNIPROT: 09ESY6	A; Cross-references: UNIPROT: Q9ESY6; GB: AF291437 A; Cross-references: UNIPROT: Q9ESY6; GB: AF291437
Thromb. Res. 53, 31-44, 1989	in protein-protein interaction and	functions as a cell adhesion molecule or soluble ligar
A;Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl A;Reference number: A60432; WUID:89162331; PMID:2922700	C;Genetics: A;Gene: nlrr-3	
A;Accession: A60432 A:Molecule twoe: nrotein	C;Keywords: cell adhesion	
A; Residues: 477-48, FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <zaf></zaf>	7.68;	Score 237; DB 2; Length 707;
Figure 1 Acad. Sci. U.S.A. 90, 8327-8331, 1993	Matches 127; Conservative 80;	Mismat
A;Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela A;Reference number: A47507; MUID:93391348; PMID:7690959	Qy 6 PLLLPLLLLLALGPGVQGCPSGCQCSQ	CPSGCQCSQPQTVFCTARQGTTVP 47
A;Accession: A47507 A:Status: preliminary: translated from GR/RMB1/DDBJ	DS S PLOIHVLEGLAITALVOAGD	: :
A; Molecule type: mRNA		
A; Cross-references: GB:L11238; NID:g388759; PIDN:AAA03069.1; PID:g388760		
C;comment: This platelet membrane protein is a substrate for thrombin. C;Comment: The amino end of the intact protein is blocked.	DB ARLPADTQILLLQINNIARI	65 AKLPADTQILLLLQITNNIAKIEHSIDFPVNLIGLDLSQNNLSSVININVQKMSQLLLSVI 122
C:Comment: This protein is absent in Bernard-Soulier syndrome. C:Genetics:	Oy 92RLPRLLLLDLS	RLPRLLLLDLS114
A;Gene: GDB:GP5	Db 123 LEENKLTELPEKCLYGLSNL	123 LEENKLTELPEKCLYGLSNLQELYVNHNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSK 182
A; Map position: Spter-Sqter C; Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot	Oy 115DTANVEALRL	
Ouerv Match 7.7%: Score 240: DB 2: Length 560:	Db 183 WFEALPNLEILMLGDNPILR	WFEALPNLEILMLGDNPILRIKDMNFQPLLKLRSLVIAGINLTEVPDDALVGLENLESIS 242
Best Local Similarity 27.2%; Pred. No. 1.2e-06; Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;	148	
NLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHN	243 FYDNRL	
	Qy 166LTRLRLAGNTRI	LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQAL-PGDLSGLFPRLR 216

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Search completed: May 12, 2005, 19:12:49
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N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42626
R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs im
A;Reference number: Z22177; MUD:99279238; PMID:10349621
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A;Residues: 1-1025 <HOL>
A;Cross-references: UNIPROT:Q9R1B9; EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AADC
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                                                                 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDDLSHNSLLALEPGILDTANVE 120
                          1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
            MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bursh J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yangura D., Godowski P.; Wood W.I., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 28, Last annotation update)
CSRV314 (Hypothetical protein LOC114990).
Name=LOC114990; ORFNames=UN0314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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SEQUENCE FROM N.A.
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A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Colline F.S., Wagger L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wckernan K.J., Malek J.A., Guarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia B., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia B., Dickson M.C.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Rakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human and mouse CDMs sequences."
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88.7%; Pred. No. 4.1e-164;
ive 0; Mismatches 1;
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EGF-like domain; Hypothetical protein.
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SMART; SM000181; EGF; 1.
SMART; SM00013; LRRUT; 1.
SMART; SM00365; LRR SD22; 4.
SMART; SM0369; LRR_TYP; 8.
PROSITE; PS01020; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01086; EGF 2; 1.
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nes 597; Conservative
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Submitted (APR-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                          891E149652DEA286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.2%; Score 3078.5; DB 2. Best Local Similarity 88.6%; Pred. No. 7.9e-164; Matches 596; Conservative 0; Mismatches 2;
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PÉAM; PF01463; LRRCT; 1.
PÉAM; PF01462; LRRNT; 1.
PÉAM; PF00560; LRR 1; 9.
PR.NTS; PR00019; LEURICHRPT.
SWART; SM00181; SGF; 1.
SWART; SM00181; LRRCT; 1.
SWART; SM0013; LRRCT; 1.
SWART; SM00365; LRRCT; 1.
SWART; SM00365; LRRCT; 1.
PROSITE; PS00129; BGF 1; 1.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS5026; BGF 2; 1.
PROSITE; PS50853; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          673 AA; 71712 MW;
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R SEQUENCE FROM N.A.

X PubMed=15247411; DOI=10.1073/pnas.0404117101;

RA Ikeda Y., Imai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,

RA Manabe II., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,

RA Manabe II., Maemura T.;

RT Sepense of Invascular semocth muscle cells, modulates the arterial

RT response to injury in vivo., I.

RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).

CC -!- SIMILARITY: Contains 1 EGF-like domain.

CC -!- SIMILARITY: Contains 1 EGF-like

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR003620; EGF_1ike.

DR InterPro; IPR003620; EGF_1ike.

DR InterPro; IPR00361; FN_III.ike.

DR InterPro; IPR003651; RN_III.ike.

DR InterPro; IPR003651; RN_III.ike.

DR InterPro; IPR003651; IRR Cterm.

DR InterPro; IPR003651; IRR LYP.
   RGRAMAAAAQDKGOVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
library, clone:0030066607 product:hypothetical Prokaryotic membrane
lipoprotein lipid attachment site/Cysteine-rich flanking region, N-
terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat,
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STRAIN-CS7BL/6J; TISSUE-Whole body;
MEDLINE-99279253; Pubmed-10349636; DOI-10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=Whole body;
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660;
RIKEN FANTOM CONSORTIUM;
"FUNCTIONAL AMNOTATION Of a full-length mouse cDNA collection.";
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Stachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Frownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Widnin T.B., Tooshiyuki S., Carninci P., Prange C.,

A Raha S.S., McKwan P.J., McKernan R.J., Maalek J.A., Gunsarene P.H.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radsiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

And Music Chia M. Ander M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.3e-142;
); Mismatches 1; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung;
Director MGC Project;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
EMBL; BCO13767; AAH13767.1; -..
HSSP; Q9BZR6; 1P8T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AA; 64178 MW; 496407F778D9ABD2 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                      rISSUE=Lung;
PubMed=12477932; DOI=10.1073/pnas.242603899;
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PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS50026; EGF 2; 1.

PROSITE; PS5083; FN3; 1.

BGF-1ike domain.

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SEOTTO
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InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003591; LRR_typ.
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InterPro; IPR006209; EGF_like.
InterPro; IPR003961; FN_III.
InterPro; IPR006210; IEGF.
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87.4%;
                                                    LOC114990 protein (Fragment)
Name=LOC114990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00181; EGF; 1.
SMART; SM00060; FN3; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00369; LRR TYP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 87.4 tes 525; Conservative
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Pfam; PF00041; fn3; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF00560; LRR 1; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences,
                                                                                            sapiens (Human)
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=9606;
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                                 STRAIN=CS7BL/6J; IISSUB=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MFDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J: TISSUE=Whole body;

MEDLINE=20530913: PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SM00181; EGF; 1.
SWART; SM00182; LRRCT; 1.
SWART; SM00082; LRRCT; 1.
SWART; SM00013; LRRUT; 1.
SWART; SM0369; LRR TYP; 3.
PROSITE; PS00124; EGF 1; UNKNOWN 1.
PROSITE; PS00126; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2177651; S11t12.
InterPro; IPR000742; EGF 2.
InterPro; IPR003509; EGF 2.
InterPro; IPR003501; FN III.
InterPro; IPR004510; IEGF.
InterPro; IPR004611; ILRR.
InterPro; IPR000483; ILRR.
InterPro; IPR000483; ILRR.
InterPro; IPR000372; ILRR. Nerm.
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Pfam; PF01462; LRRNT; 1.
Pfam; PF00560; LRR 1; 8.
PRINTS; PR00019; LEURICHRPT.
Nature 409:685-690(2001)
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Pfam; PF00041; fn3; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           91 -----LRLPRLLLLDLSHNSLLALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 PGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 GEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCVRRARA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 AAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606 TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGBALSGGPECEVPLMGYPGPSLQG
                                                                                                                                  Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                78;
                                                                                          Length 673;
                                                                                                                                  Indels
PROSITE; PS50853; FN3; 1.
EGF-like domain; Hypothetical protein; Lipoprotein.
SEQUENCE 673 AA; 72284 MW; E35D1B35DDFF5EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
25-CT-2004 (TrEMBLrel. 28, Last annotation update)
Slit-like 2 protein precursor.
                                                                                   79.5%; Score 2491; DB 2; 73.5%; Pred. No. 4.7e-131; ive 25; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 AA
                                                                                                                                                                                                                                                                  66 MLDASSFAGLPGLQLLDLSQNQIAS----
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                                                                                 Query Match
Best Local Similarity 73.5:
Matches 491; Conservative
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SEQUENCE FROM N.A.
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01-JUN-2002 (
01-JUN-2002 (
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367 REPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTWRPAPQPQDCPASICLNGGSCRLGAR 426
                                                                                                                   LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNPFNCLCP
                                                                                    -- LRLPRLLLLDLSHNSLLALE
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STRAIN=CS7BL/6J; TISSUB=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Musm.2004 (TrEMBLrel. 26, Last annotation update)
Musm.sculus 10 days embryo whole body CDNA, RIKEN full-length
enriched library, clone:32410528605 product:hypothetical Prokaryotic
membrane lipoprotein lipid attachment site/Cysteine-rich flanking
region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich
repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich
flanking region, C-terminal/Leucine-rich region/Fibronectin type III
domain containing protein, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=Whole body;
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                                                                                                  STRAIN=FVB/N; TISSUE=Kidney;

XX STRAIN=FVB/N; TISSUE=Kidney;

XX STRAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Staueberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

XX Riausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

Altschul S.F.; Zeeberg B., Buerow K.H.; Schaefer C.F.; Bhat N.K.;

XX Altschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haith F.;

XX Altschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haith F.;

XX Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

XX Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

XX Bosak S.A.; McEwan R.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

XX Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

XX Villaton D.K.; Muzny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.;

XX Helton E.; Ketreman M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

XX Rizzywinski M.I.; Skalska U.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

XX Jones S.J.; Marra M.A.;

XX JONES S.J.;

XX JONE
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     E.;
to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
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AAB8DA82DA8E9D32 CRC64;
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EMBL; AJ458938; CAD30331.1; -.
EMBL; BCD60274; AAH50274.1; -.
EKSP; P00740; 1EDM.
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PS00022; EGF 1; UNKNOWN 1.
PS01186; EGF 2; 1.
PS50026; EGF 3; 1.
PS50083; FN3; 1.
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InterPro; IPR000742; EGF 2.
InterPro; IPR000399; EGF 2.
InterPro; IPR003961; FN III.
InterPro; IPR006210; IEGF.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR.
InterPro; IPR000372; LRR.
InterPro; IPR00372; LRR.
InterPro; IPR00372; LRR.
InterPro; IPR00372; LRR.
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SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR TYP;
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Pfam; PF01462; LRRNT; 1.
Pfam; PF00560; LRR 1; 8.
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EGF-like domain; Signal.
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SMART; SM00060; FN3; 1.
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Pfam; PF00041; fn3; 1.
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PROSITE; PS00022; EGF
PROSITE; PS01186; EGF
PROSITE; PS50026; EGF
     Schrewe H., Kutejova
Submitted (APR-2002)
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Arakawa T., Azahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kosuka T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito R., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagawi M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (UIL-2000) to the EMBL/GenBank/DDBJ databases.
- SIMILANITY: Contains 1 EGF-like domain.
R EMBL, AKO12169; BAB28075.1;
- HSSP; P00740; IEDM.
                                                                                                                     Team;
annotation of
                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/64); TISSUE-Whole body; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Yatsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwke S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Foneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500; RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                 STRAIN=C1700 And TISSUE-Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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InterPro; IPR000483; LRR Cterm.
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR typ.
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InterPro; IPR00742; BGF_2.
InterPro; IPR005209; BGF_like.
InterPro; IPR003961; FN_III.
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LEURICHRPT.
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; SM00060; FN3; 1.
; SM00082; LRRCT; 1.
; SM00013; LRRNT; 1.
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                                              Nature 409:685-690(2001)
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PF01462; LRRNT; 1.
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                                                                                                                                                                                            SEQUENCE FROM N.A.
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Pfam; PF00041;
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SMART;
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                                                                                                                                                                                                                                                                                            9 FLL--LILLVLLGSGVQGCPSGCQCNQPQTVFCTARQGTTVFRDVFPTVGLYIFENGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 LSWFGPWVRENHVVLASPEETRCHFPFKNAGRLLLDLDYADFGCFVTTTTATVPTIRSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 HHWECLCPEGFIGLYCESPVEQGMKPSSIPDIPRPPPLLPLSIEPVSPTSLRVKLQRYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                  78;
                                                                                                                                                                    Length 673;
                                                                                                                                                                                                                  Indels
                                                                                            domain; Hypothetical protein; Lipoprotein. 673 AA; 72336 MW; 9C53F90ADF43FBD9 CRC64;
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Last annotation update)
                                                                                                                                                              Query Match 79.2%; Score 2484; DB 2; Best Local Similarity 73.4%; Pred. No. 1.2e-130; Matches 490; Conservative 25; Mismatches 75;
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PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
PS50026; EGF_3; 1.
PS50853; FN3; 1.
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Q6PJG9
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                                              TISSUE-Whole body.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (ULL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
EMBL, BC076888; AH7768881; -.
InterPro; IPR008985; ConA, like_lec_gl.
InterPro; IPR00742; EGF \(\bar{2}\)
InterPro; IPR005709; EGF \(\bar{2}\)
InterPro; IPR005209; EGF \(\bar{2}\)
InterPro; IPR005210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 AA; 71957 MW; A0AC47946BE8DBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SMART; SM00369; LRR_TYP; 6.
PROSITE; PS00022; BGF_1; UNKNOWN_1.
PROSITE; PS50026; BGF_2; 1.
BGF-11ke domain.
SEQUENCE 661 AA; 71957 WW; AOAC47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003885; LRR_cyst.
InterPro; IPR003591; LRR_typ.
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SMART; SM00082; LRRCT; 1.
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Pfam, PF01463, LRRCT; 1.
Pfam, PF00560, LRR_1; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences.
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Klein S., Gerhard D.S.;
Submitted (JUL-2004) to
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MEDINE-2038825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-2038825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Gohnler G.D.,
A Lischul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,
A Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Weders G.J., Abramson R.D., Millahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Muzny D.M., Sodergren B.D., Dickson M.C.,
A Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Gones S.J., Marra M.A.,
A Mones S.J., Marra M.A.,
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                                        409 PQTCLNGGSCHLDPTGQLECECPPGFQGTYCET------GPVTPAVVTEMYIEQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 IEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRP
LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPFNCVCP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Leucine rich repeat and fibronectin type III domain containing
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SEQUENCE FROM N.A.
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NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : || || || || 61 QALGPPDFRNMTGLVDLTLSRNAITRIGARAFGDLESLRSLHLDGNRLVELGTGSLRGPV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 NVEALRIAGLGLQQLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR-----LLAAARNPFN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 -IDALPPGAFAQLGQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPAPLVLSFSGNPLH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPRSI----TLGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKRLVTL 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLPLLLLLALGPGVQGCPSGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 359.5; DB 2; Length 635; 27.6%; Pred. No. 3.8e-12; ive 61; Mismatches 281; Indels 101;
                                            to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66859 MW; 13E66645A17A92EE CRC64;
                                                           EMBL; BC015581; AAH15581.2; InterPro; IPR003961; FN III. InterPro; IPR003199; Ig. InterPro; IPR007110; Ig-like. InterPro; IPR007110; Ig-like. InterPro; IPR00710111; IRR. InterPro; IPR000483; IRR Cterm. InterPro; IPR000483; IRR Cterm. InterPro; IPR000483; IRR Cterm. InterPro; IPR001611; IRR CTERM. INTERPO; IPR001611; IRR CTERM. INTERPO; IPR001611; IRR CTERM.
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PRINTS; PR00019; LEURICHRPT.
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PROSITE; PS50835; IG LIKE
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SM00369; LRR TYP;
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SMART; SM00409; IG; 1.
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                     Strausberg R.;
Submitted (OCT-2001)
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachine J.C., Feingold E.A., Grouse L.H., Derge J.G.,

Altachine S.P., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B commercia M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B romantein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Mones S.J., Marra M.A.,

"Mones S.J., Marra M.J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAPPLILLILLASGAAACPLPCVCONLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI
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                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Leucine rich repeat and fibronectin type III domain containing 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Eye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0019; LEURICHRPT.
PROSITE; PS50835; FN3; 1.
SROUTE; PS50835; IG LIKE; 1.
SROUTE 636 AA, 67251 MW; 1EE86E96CB8BA91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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989
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Straubberg R.;
Submitted (FRB-2002) to the Err
EMBL; BC023036; AAH23036.1; -
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InterPro; IPR007110; Ig-like.
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InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 27.2°
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00041; fn3; 1.
Pfam; PF00560; LRR 1; 6
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
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TMLDASSFAGLPGLQLLDLSQNQIASL-----RLPRLLLLLDLSHNSLLAL-EPGILDTA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 -IDALPPGVFAQLSQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTLRLPASLAEYTVTOLRPNATYSVCVMPLGPGRVPEGEEA-----CGEAHTPPAVHSN 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAPPLILILIZASGAAACPLPCVCQNISESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QALGPPDFRNMTGLVDLTLSRNALTRIGARSFGDLESLRSLHLDGNRLVELGSSSLRGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVEALRLAGIGLOOLDEGLFSR-LRNLHDLDVSDNOLERVP-PVIRGLRGLTRLAGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EPPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG-----PDDRLVGNSSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM-------GQGTRPSPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 WAFPNGTLEIGVTGAGDAGAYTCIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTPRPPRSL----TLGIEP----VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 IAASARTAAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIQYN--SSEDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIYRIVPASSHHFLLKHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPANPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPQPQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HALQAHVLGGTLTV----AVGGVLVAALLVFTVALLV-RGRG------AGNGRLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LLPLLLLLALGPGVQGCPSGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.1%; Score 348; DB 2; Length 636; Best Local Similarity 27.2%; Pred. No. 1.7e-11; Matches 170; Conservative 62; Mismatches 276; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCELLWLR-----RLARPDDLETCASPPTLAGRYFWAVPEGEFSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9CE86E8A3981A884 CRC64;
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InterPro; IPR003961; FN III.
InterPro; IPR00110; Ig-like.
InterPro; IPR001598; Ig-c2.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR.Cterm.
InterPro; IPR000372; LRR Merm.
InterPro; IPR00372; LRR Werm.
InterPro; IPR00373; LRR CFrm.
InterPro; IPR00373; LRR CFrm.
InterPro; IPR003591; LRR Lyp.
Ffam; PF00641; Fn3; 1.
                                                                                                                                                                                                                                                                                                                SWART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00082; LRRCT; 1.
SWART; SM00013; LRRNT; 1.
SWART; SM00369; LRR_TYP; 2.
PROSITE; PSS0853; FN3; 1.
PROSITE; PSS0835; IG_LKE; 1.
SEQUENCE 636 AA; 67264 MW; 91
                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT
  AAH23156.1;
                           Q9BZR6;
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Q8BLU0
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                                                                                                                                                                                    -----BPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG----PDDRLVGNSSRA 328
                                                                                                                                           286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPQPQD------ 333
                                                                                                                                                                                                                                              ----GQGTRPSPTP 380
                                                                                                                                                                                                                                                                                          329 WAFPNGTLEIGVTGAGDAGAYTĆIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD 388
                                                                                                                                                                                                                                                                                                                                          381 VTPRPPRSL----TIGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR 432
                                                                                                                                                                                                                                                                                                                                                                                             389 IAASARTAAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIQYN--SSEDET 446
                                                                                                                                                                                                                                                                                                                                                                                                                                             LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA-----CGEAHTPPAVHSN 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 LIYRIVPASSHHFLLKHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPATFLC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPL 547
-IDALPPGVFAQLSQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237
                                                CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLLELDYADFGCPATTTTATVPT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 HALQAHVLGGTLTV----AVGGVLVAALLVFTVALLV-RGRG------AGNGRLPL 551
                                                                                              CNCELLWIR-----RLARPDDLETCASPPTLAGRYFWAVPEGEFSC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            334 -CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 KLSHVO----SOTNGGTSPMP 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 ELEGVKVPLEPGPKATEGGGEALP 571
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Name=Lrfn4;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6xCBA;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
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Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Soqabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus adult male aorta and vein cDNA, RIKEN [All-length
enriched library, clone.45310098L04 product:KTAA0405 (LEUCINE-RICH
REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasakin N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
  660 AA.
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STRAIN=CS7BL/6J; TISSUE=Aorta and vein;
The FANTOM Consortium,
                                                Created)
                                                                                                                                                                                                                    Name=Map4k5; Synonyms=Flrt2;
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PRELIMINARY;
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308 RNNPWFCDCSIKWYTEWIKYIPSSL-NVRGFMCQGPEQVRGMAVRELNMNLLSCPTTTPG 366
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   Rigby P.W.J.;
EMBL/GenBank/DDBJ databases.
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InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR_typ.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00041; fn3; 1.
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PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
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GO; GO:0016021; C:integral to
InterPro; IPR003961; FN III.
InterPro; IPR001611; LRR.
Haines B.P., Summerbell D.,
Submitted (DEC-2003) to the
EMBL; AKO41311; BAC30900.1;
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Pfam; PF00560; LRR_1; 10.
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493 LVPLDAFNYRTVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGLIGGAV 551
                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
library, clone:C230002N12 product:hypothetical Zinc carboxypeptidases,
carboxypeptidase A metalloprotease (M14) family containing protein,
full insert sequence (Mus musculus adult male olfactory brain cDNA,
RIKEN full-length enriched library, clone:6430402H13
product:hypothetical Zinc carboxypeptidases, carboxypeptidase A
metalloprotease (M14) family containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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SEQUENCE FROM N.A.
STRANN=C57BL/6J; TISSUB=Cerebellum, and Olfactory brain;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-C57BL/60; TISSUE-Cerebellum, and Olfactory brain; MEDLINE-2050913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabliwagi K., Fujiwake S., Inoue K., Tozawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";
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                                                                           512 LAALAAVGAAYC---VRRGR 528
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                                                                                                                                            552 IFVLVVLLSVFCWHMHKKGR
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

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RATH=C57BL/6J; TISSUE=Olfactory brain;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,

Rukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Indocani K., Ishii Y., Itoh M., Kagawa I., Kauda M.,

Ratoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,

Ratoh H., Kawai J., Kojima Y., Myazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N., Sano H.,

Rayawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Rumi, AKO48678; BAC334191; -.

BMBL, AKO78176; BAC331191; -.

REMBL, AKO78176; BAC331191; -.

REMBL, AKO78176; BAC31163.1; -.
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Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Furuno M., Hanagaki T., Haraka T., Hirozane T., Horibar B., Furuno M., Haramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibate K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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R InterPro; IPR001599; IG_C2.
R InterPro; IPR001599; IG_C2.
R InterPro; IPR001591; ILRR.
R InterPro; IPR001591; ILRR.
R InterPro; IPR000372; ILRR.
R InterPro; IPR000372; ILRR.
R Pfam; PF00163; ILRR.
R Pfam; PF00169; ILRR.
R PRINTS; PR00019; ILRR.
R SMART; SM00081; ILRR.
R SMART; SM00082; ILRR.
R SMART; SM00083; ILRR.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS50835; IG_LIKE; 1.
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GO; GO:0004180; F:carboxypeptidase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
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Matches 149; Conservative
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169 IRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLKLLAAARNPFNCV 228
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                                                                    --- ENGITMLDASSFAGLPGLQL
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   LLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF----
                                   3 LYLQVSKLLA-----CPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLYLHNNQINN
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MEDLINE=22897296; POI=10.1101/gr.1293003;
MEDLINE=22897296; Pubmed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Thesis (2000), Zhongshan Medical University / Guangzhou, China
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"Brain-specific gene, a novel member of leucine rich rep
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9HBMI, OGZNIB; O96ABS; 25-OCT-2004 (Rel. 45, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 25-OCT-2004 (Rel. 45, Last sequence update) Leucine-rich repeat-containing protein 4 precursor associated protein LRRC4) (NAG14) (UNQ554/PRO1111). Homo sapiens (Human).
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537 SVFCWHMHKKGR 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 AAYC---VRRGR
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                                                                    61 -----
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                 --IP 267
                                                 285 TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPP--STCLNG 342
                                                                          268 PSVNV--EPPEFTANLGED-LQVACQASGYPQP----LVVWRKVPQPRDGKPQAQAQLEG 320
                                                                                                                343 GTCHLG------TRHHLACLCPEGFTGLY-CESQMGQGTRPSPTPVTPRPPR 387
                                                                                                                                                                                     436
                                                                                                                                                                                                       : : : | : | : | : | : | 375 QQSQQLPDPQAPATRPVGHEPQHEAGSWAFRALGLATQTAITAAIALLALITALLLAAMIC 434
                                                                                                                                                                                                                                                      ----VTQLRPNATYSVCVM----PLGPGRVPE 470
                                                                                                                                                                                                                                                                          321 GAPGLGGHGTRDTGSGMLFLTNITLA-----HAGKYECEAANAGGKARVPFHLLVNASR
                                                                                                                                                                                   388 SLTLGI-EPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H., Koga H., Frediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous CDNAs Identified by Screening of Terminal Sequences of cDNA Clones Enandomly Sampled from Size-Fractionated Libraries.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
216 CDCALHWIGSWIKEGGRRLLSSRDKKITCAEPPRLALQSLLEVSGGSLIC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AKT72945, BAD32223.1; --
INTERPRO; IPR003961; FN III.
INTERPRO; IPR003957; FN III-like.
INTERPRO; IPR0004611; LRR.
INTERPRO; IPR000431; LRR. Cterm.
INTERPRO; IPR000372; LRR.Nterm.
INTERPRO; IPR0013591; LRR. LYP.
INTERPRO; IPR001211; PhoSpholipaseA2.
PÉam; PF00041; Én3; 1.
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PROSITE; PS00119; PA2 ASP; UNKNOWN 1.
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PRINTS; PR00019; LEURICHEPT.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 7.
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Matches 142; Conservative
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RR SECUBRICE FROM N.A.

RA WARAMEND A., Hayaabi K., Sarch H., Nagai K., Kimura K., Makita H.,

RA WARAMEND A., Hayaabi K., Sarch H., Magai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Dayashi M., Nawai Y., Isono Y., Nakamura Y.,

RA Sekine M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

RA Shiratori A., Zudo H., Hosoiri T., Kaku Y., Kodaira H., Rondo H.,

RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa K.,

RA Tanazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Tanazaki M., Ninomiya K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Takajuguchi S., Watanabe S., Yoshida M., Aoteuka S.,

RA Nomiya S., Momiyama H., Satoh N., Takami S., Terashima Y., Sano S.,

Musashino K., Watanabe T., Sugiyama A., Sanski N., Aoteuka S.,

RA Yoshikawa Y., Matanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Jimori Y., Komiyama M., Tashiro M., Takama Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Angawa S., Senoh T., Sujima A., Takahashi Y., Nakagawa K.,

RA Aogashi T., Oyama M., Hara H., Watanabe M., Komateu T.,

RA Matsumura K., Nakajima Y., Mizuno T., Moringa M., Sasaki M.,

A Rasinkani Y., Yada T., Noguchi S., Toh, Takahashi Y., Nakagawa K.,

RA Aogashi T., Oyama M., Hara H., Watanabe M., Komateu T.,

RA Aogashi T., Yada T., Noguchi S., Toh, Takahashi Y., Nakajawa K.,

RA Aogashi T., Yada T., Noguchi S., Tokhi H., Masuho Y., Yamashita R.,

A Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Complete sequencing and characterization of 21,243 full-length human
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                         "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 36:40-45(2004).
--- SUBCELLIOLAR LOCATION: Type I membrane protein (Potential).
--- SIMILARITY: Contains I immunoglobulin-like domain.
--- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                       bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Pfam; PF00047; ig; 1.
Pfam; PF01560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR001019; LEURICHRPT.
PROSITE; PS50835; IG LIKE; 1.
Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR0001611; LRR.
InterPro; IPR000372; LRR Vterm.
InterPro; IPR003591; LRR_VPP.
                                                   EMBL; AJ297858; CAC82651.1; -. EMBL; AF196976; AAG28019.2; -.
                                                                                                       EMBL, AY358307; AAQ88674.1; --
EMBL, AK172751; BA118737.1; --
HSSP, Q9BZR6; 1P8T.
Genew, HGNC.15586; LRRC4.
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77 TRYLNLMENNIQMIQMIQMDTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLNTLELFDNWLT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 PWVRESHVTLASPEETRCHPPPKNAGRLLLELDYADFGCPATTTTTATVPTTRPVVREPTA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 SEGRMA------ELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGT--LNFSH 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 TVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLR-----LPRLLLLDDLSHNSLL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 ALEPGILDTAN-----LOQLDEGLESRLR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA---RNPFNCVCPLSWFG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMP----- 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : | | : : | | STAELNTSNYSFFT-----TVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVL 494
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                                        Leucine-rich repeat-containing protein 4. Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 NLKYLNLGMCNIKDMPNLTPLVCLEELEMSGNHPPEIRPGSFHGLSSLKKLWVM-NSQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLPLLLL------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 LSSSLAPTWLSPTAPATEAPSPPSTAPPTVGP----VPQPQDCPPSTCLNGGTCHLGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 HLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TCMVTNVAGNS---NASAYLNV
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24.3%; Pred. No. 1.7e-10;
tive 82; Mismatches 245; Indels 168; Gaps
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(Potential).
(Potential).
(Potential).
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                                                                                                          Cytoplasmic (Potential)
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QVSLI -> H (in Ref. 1).

N -> D (in Ref. 4).

L -> F (in Ref. 4).
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Signal; Transmembrane
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